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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:02:07 ; Search time 12.3745 Seconds  
(without alignments)  
3219.466 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:  
1: geneseqp1980s:  
2: geneseqp1990s:  
3: geneseqp2000s:  
4: geneseqp2001s:  
5: geneseqp2002s:  
6: geneseqp2003as:  
7: geneseqp2003bs:  
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	680.5	96.5	522	3	AAY71312	Aay71312 Rat neuri
2	510	72.3	199	5	ABB81077	Abb81077 Rat neuro
3	503	71.3	118	5	ABB89192	Abb89192 Human pol
4	503	71.3	199	2	AAW53947	Aaw53947 Human NSP
5	503	71.3	199	2	AAW78313	Aaw78313 Fragment
6	503	71.3	199	2	AAY35903	Aay35903 Extended
7	503	71.3	199	3	AAB12805	Aab12805 Human NSP
8	503	71.3	199	4	AAB82348	Aab82348 Human NOG
9	503	71.3	199	5	ABG30939	Abg30939 Human Nog

10	503	71.3	199	5	ABB81080	Abb81080 Human neu
11	499.5	70.9	199	3	AAY71559	Aay71559 Rat Nogo
12	448	63.5	1178	3	AAY71311	Aay71311 Human neu
13	447	63.4	403	3	AAY71563	Aay71563 Rat Nogo
14	447	63.4	893	3	AAY95012	Aay95012 Human sec
15	447	63.4	983	6	ABU11573	Abu11573 Human MDD
16	447	63.4	1162	3	AAY71557	Aay71557 Rat Nogo
17	447	63.4	1163	3	AAY71310	Aay71310 Rat neuri
18	447	63.4	1163	3	AAY71384	Aay71384 Alternati
19	447	63.4	1163	5	ABB81074	Abb81074 Rat neuro
20	447	63.4	1192	3	AAY56967	Aay56967 Human MAG
21	447	63.4	1192	4	AAB82349	Aab82349 Human NOG
22	447	63.4	1192	4	AAU04591	Aau04591 Human Nog
23	447	63.4	1192	5	ABG30938	Abg30938 Human Nog
24	447	63.4	1192	5	ABP68600	Abp68600 Human pan
25	447	63.4	1192	5	ABB81078	Abb81078 Human neu
26	447	63.4	1192	6	ABR59667	Abr59667 Human Nog
27	443	62.8	103	4	AAE03980	Aae03980 Human gen
28	443	62.8	200	4	AAB64514	Aab64514 Human sec
29	443	62.8	359	3	AAY71558	Aay71558 Rat Nogo
30	443	62.8	360	3	AAY71383	Aay71383 Rat neuri
31	443	62.8	360	4	AAE03987	Aae03987 Human gen
32	443	62.8	360	5	ABB81076	Abb81076 Rat neuro
33	443	62.8	361	3	AAY71385	Aay71385 Alternati
34	443	62.8	373	3	AAY53624	Aay53624 A bone ma
35	443	62.8	373	3	AAY56969	Aay56969 Human MAG
36	443	62.8	373	3	AAB24242	Aab24242 Human Nog
37	443	62.8	373	4	AAB82350	Aab82350 Human NOG
38	443	62.8	373	5	AAM47954	Aam47954 Human RTN
39	443	62.8	373	5	ABG30937	Abg30937 Human Nog
40	443	62.8	373	5	ABP68601	Abp68601 Human pan
41	443	62.8	373	5	ABB81079	Abb81079 Human neu
42	443	62.8	379	7	ADB85283	Adb85283 Rat fooce
43	440	62.4	91	2	AAY12360	Aay12360 Human 5'
44	439	62.3	291	4	AAM93484	Aam93484 Human pol
45	410.5	58.2	642	2	AAW58383	Aaw58383 Human sec

#### ALIGNMENTS

RESULT 1

AAY71312

ID AAY71312 standard; protein; 522 AA.

XX

AC AAY71312;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo C.

XX

KW Rat; neurite growth inhibitor; Nogo C; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.  
XX  
OS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT Region 1. .39  
FT /note= "Sequence upstream to the N-terminus of Nogo C  
FT protein"  
FT Misc-difference 3  
FT /note= "Encoded by TAG"  
FT Region 11. .191  
FT /note= "Region specifically described in claim 16"  
FT Misc-difference 29  
FT /note= "Encoded by TAA"  
FT Protein 40. .238  
FT /label= Nogo\_C\_protein  
FT Region 51. .238  
FT /note= "C-terminal common region found in Nogo A, B and C  
FT isoforms "  
FT Region 239. .522  
FT /note= "Sequence downstream to the C-terminus of Nogo C  
FT protein"  
FT Misc-difference 239  
FT /note= "Encoded by TGA"  
FT Misc-difference 263  
FT /note= "Encoded by TGA"  
FT Misc-difference 276  
FT /note= "Encoded by TAG"  
FT Misc-difference 281  
FT /note= "Encoded by TGA"  
FT Misc-difference 295  
FT /note= "Encoded by TAA"  
FT Misc-difference 298  
FT /note= "Encoded by TAA"  
FT Misc-difference 314  
FT /note= "Encoded by TGA"  
FT Misc-difference 318  
FT /note= "Encoded by TGA"  
FT Misc-difference 335  
FT /note= "Encoded by TAG"  
FT Misc-difference 371  
FT /note= "Encoded by TGA"  
FT Misc-difference 374  
FT /note= "Encoded by TAG"  
FT Misc-difference 380  
FT /note= "Encoded by TAA"  
FT Misc-difference 406  
FT /note= "Encoded by TAA"  
FT Misc-difference 408  
FT /note= "Encoded by TAG"  
FT Misc-difference 410  
FT /note= "Encoded by TAA"  
FT Misc-difference 422  
FT /note= "Encoded by TAA"  
FT Misc-difference 433  
FT /note= "Encoded by TGA"  
FT Misc-difference 440

FT /note= "Encoded by TAG"  
FT Misc-difference 453  
FT /note= "Encoded by TAG"  
FT Misc-difference 465  
FT /note= "Encoded by TAG"  
FT Misc-difference 482  
FT /note= "Encoded by TAG"  
FT Misc-difference 513  
FT /note= "Encoded by TAA"  
XX  
PN WO200031235-A2.  
XX  
PD 02-JUN-2000.  
XX  
PF 05-NOV-1999; 99WO-US026160.  
XX  
PR 06-NOV-1998; 98US-0107446P.  
XX  
PA (SCHW/) SCHWAB M E.  
PA (CHEN/) CHEN M S.  
XX  
PI Schwab ME, Chen MS;  
XX  
DR WPI; 2000-400052/34.  
DR N-PSDB; AAD01175.  
XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX  
PS Claim 7; Fig 14; 122pp; English.  
XX  
CC The present sequence is a rat Nogo C protein which is a potent neural  
CC cell growth inhibitor and is free of all central nervous system (CNS)  
CC myelin material with which it is natively associated. Nogo proteins and  
CC fragments displaying neurite growth inhibitory activity are used in the  
CC treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
CC haemangioblastoma, acoustic neuroma, oligodendrogloma, menangioma,  
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
CC activity can be used to treat or prevent hyperproliferative or benign  
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
CC production of Nogo protein to induce regeneration of neurons or to  
CC promote structural plasticity of the CNS in disorders where neurite  
CC growth, regeneration or maintenance are deficient or desired. The animal  
CC models can be used in diagnostic and screening methods for predisposition  
CC to disorders and to screen for or test molecules which can treat or  
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However the specification does not include sequences for  
CC these SEQ ID numbers  
XX  
SQ Sequence 522 AA;

Query Match 96.5%; Score 680.5; DB 3; Length 522;  
Best Local Similarity 98.6%; Pred. No. 2.5e-71;

Matches 138; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 3 SGEAGVSCLRENFAVYSVGMHNL-LLEGRSWQEMDGQKKHWKDKVVVDLLYWRDIKKT 61  
| |||||||  
Db 4 SGEAGVSCLRENFAVYSVGMHNLXLLLEGRSWQEMDGQKKHWKDKVVVDLLYWRDIKKT 63  
| |||||||  
QY 62 GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYL 121  
| |||||||  
Db 64 GVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYL 123  
| |||||||  
QY 122 ESEVAISEELVQKYSNSALG 141  
| |||||||  
Db 124 ESEVAISEELVQKYSNSALG 143

## RESULT 2

ABB81077

ID ABB81077 standard; protein; 199 AA.

XX

AC ABB81077;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-C.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
KW central nervous system; peripheral nervous system; tranquilizer; Nogo;  
KW vulnerability; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.  
PR 21-JUL-1998; 98WO-US014715.  
PR 22-DEC-1998; 98US-00218277.  
PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA ) YEDA RES &amp; DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;

PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in the  
PT central/peripheral nervous system from injury/disease, comprises  
PT administering nervous system-specific activated T cells/antigen, or  
PT analogs/peptides.

XX  
PS Example 5; Page 48-49; 93pp; English.  
XX  
CC The invention relates to promoting nerve regeneration or conferring neuroprotection and preventing or inhibiting neuronal degeneration in the central/peripheral nervous system (NS). The method involves administering NS-specific activated T cells, NS-specific antigen, its analogue or its peptide, a nucleotide sequence the NS-specific antigen or its analogue or combinations. The method is useful for promoting nerve regeneration and preventing neuronal degeneration in central/peripheral nervous system from injury/disease, where the injury is spinal cord injury, blunt trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or damages caused by surgery such as tumour excision. The disease is not an autoimmune disease or neoplasm. The disease results in a degenerative process occurring in either gray or white matter or both. The disease is diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea, amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and vitamin deficiency, intervertebral disc herniation, prion diseases such as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral neuropathies associated with various diseases, including but not limited to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary amyloidosis, obstructive lung diseases, acromegaly, malabsorption syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-pathies, complications of various drugs (e.g., metronidazole) and toxins (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia telangiectasia, Friedreich's ataxia, amyloid polyneuropathies, adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's disease, or lipoproteinemia. The present sequence represents the rat neurotransmitter receptor protein Nogo-C, an example of NS-specific antigen  
XX  
SQ Sequence 199 AA;

Query Match 72.3%; Score 510; DB 5; Length 199;  
Best Local Similarity 99.0%; Pred. No. 9.6e-52;  
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 38 MDGQKKHWKDKVV DLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 1 MDGQKKHWKDKVV DLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
  
Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 3  
ABB89192  
ID ABB89192 standard; protein; 118 AA.  
XX  
AC ABB89192;  
XX  
DT 24-MAY-2002 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 1568.

XX  
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO200190304-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 18-MAY-2001; 2001WO-US016450.  
XX  
PR 19-MAY-2000; 2000US-0205515P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Birse CE, Rosen CA;  
XX  
DR WPI; 2002-122018/16.  
DR N-PSDB; ABL89601.  
XX  
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
PT prevention of neural, immune system, muscular, reproductive,  
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
PT disorders.  
XX  
PS Claim 11; SEQ ID NO 1568; 2081pp + Sequence Listing; English.  
XX  
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins  
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating  
CC medical conditions e.g. by protein or gene therapy. The genes are  
CC isolated from a range of human tissues disclosed in the specification.  
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)  
XX  
SQ Sequence 118 AA;

Query Match 71.3%; Score 503; DB 5; Length 118;  
Best Local Similarity 98.1%; Pred. No. 3.2e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 MDGQKKNWKDKVVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
QY 98 FRIYKGVIQAIAKSDEGHFRAYLESEVAISEELVQKYSNSALG 141  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 61 FRIYKGVIQAIQKSDEGHFRAYLESEVAISEELVQKYSNSALG 104

RESULT 4

AAW53947

ID AAW53947 standard; protein; 199 AA.

XX

AC AAW53947;

XX

DT 24-JUL-1998 (first entry)

XX

DE Human NSPLP protein A.

XX

KW NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;  
KW neurodegenerative disease; amyotrophic lateral sclerosis; cancer.

XX

OS Homo sapiens.

XX

PN WO9806841-A2.

XX

PD 19-FEB-1998.

XX

PF 24-JUL-1997; 97WO-US013469.

XX

PR 12-AUG-1996; 96US-00700607.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Bandman O, Au-Young J, Goli SK, Hillman J;

XX

DR WPI; 1998-159533/14.

DR N-PSDB; AAV23695.

XX

PT Human neuro-endocrine-specific protein-like proteins - useful for  
PT diagnosis, monitoring and treatment of cancer and neuro-degenerative  
PT disease.

XX

PS Claim 1; Page 38; 73pp; English.

XX

CC This sequence is a human neuroendocrine-specific protein-like protein  
CC (NSPLP) of the invention. Recombinant cells transformed with the DNA are  
CC used to express the NSPLP proteins, which are used to treat cancer and  
CC neurodegenerative diseases such as amyotrophic lateral sclerosis. Also  
CC antisense nucleic acids and antagonists of NSPLP can be used to inhibit  
CC activity of the NSPLP proteins. Antibodies specific for NSPLP are used  
CC for diagnosis and monitoring treatment of diseases associated with NSPLP  
CC expression, in usual immunoassays, and to isolate NSPLP from natural  
CC sources. The NSPLP proteins, or their fragments can also be used in drug  
CC screening to identify NSPLP antagonists. The nucleic acid can be used  
CC diagnostically and for monitoring treatment (in hybridisation or  
CC amplification assays); to isolate closely related sequences; in gene  
CC therapy for both sense and antisense applications (including use of  
CC ribozymes) and for mapping the natural genomic sequence



PR 18-AUG-1997; 97US-0055984P.  
PR 12-SEP-1997; 97US-0058665P.  
PR 12-SEP-1997; 97US-0058668P.  
PR 12-SEP-1997; 97US-0058669P.  
PR 12-SEP-1997; 97US-0058750P.  
PR 12-SEP-1997; 97US-0058971P.  
PR 12-SEP-1997; 97US-0058972P.  
PR 12-SEP-1997; 97US-0058975P.  
PR 02-OCT-1997; 97US-0060834P.  
PR 02-OCT-1997; 97US-0060841P.  
PR 02-OCT-1997; 97US-0060844P.  
PR 02-OCT-1997; 97US-0060865P.  
PR 02-OCT-1997; 97US-0061059P.  
PR 02-OCT-1997; 97US-0061060P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;  
PI Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;  
PI Feng P;

XX

DR WPI; 1999-080881/07.

DR N-PSDB; AAX04379.

XX

PT New isolated human genes and the secreted polypeptides they encode -  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.

XX

PS Disclosure; Page 62; 380pp; English.

XX

CC This sequence represents a fragment of a secreted human protein encoded  
CC by the nucleic acid molecule detailed in the descriptor line. The gene  
CC can be used to generate fusion proteins by linking to the gene to a human  
CC immunoglobulin Fc portion (e.g. AAX04302) for increasing the stability of  
CC the fused protein as compared to the human protein only. The invention  
CC relates to 86 novel genes and their fragments (nucleic acid sequences:  
CC AAX04311-X04410; amino acid sequences AAW78126-W78225) which are useful  
CC for preventing, treating or ameliorating medical conditions e.g. by  
CC protein or gene therapy. Also, pathological conditions can be diagnosed  
CC by determining the amount of the new polypeptides in a sample or by  
CC determining the presence of mutations in the new polynucleotides.  
CC Specific uses are described for each of the 86 polynucleotides, based on  
CC which tissues they are most highly expressed in (see AAX04311 for  
CC described uses)

XX

SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 2; Length 199;  
Best Local Similarity 98.1%; Pred. No. 6.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db

61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 6

AAY35903

ID AAY35903 standard; protein; 199 AA.

XX

AC AAY35903;

XX

DT 13-SEP-1999 (first entry)

XX

DE Extended human secreted protein sequence, SEQ ID NO. 152.

XX

KW Secreted protein; human; cytokine; cellular proliferation; cell movement;  
KW cellular differentiation; immune system regulator; anti-inflammatory;  
KW haematopoiesis regulator; tissue growth regulator; tumour inhibitor;  
KW reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;  
KW genetic disease.

XX

OS Homo sapiens.

XX

PN WO9931236-A2.

XX

PD 24-JUN-1999.

XX

PF 17-DEC-1998; 98WO-IB002122.

XX

PR 17-DEC-1997; 97US-0069957P.

PR 09-FEB-1998; 98US-0074121P.

PR 13-APR-1998; 98US-0081563P.

PR 10-AUG-1998; 98US-0096116P.

XX

PA (GEST ) GENSET.

XX

PI Bougueret L, Duclert A, Dumas Milne Edwards J;

XX

DR WPI; 1999-385906/32.

DR N-PSDB; AAX97587.

XX

PT New isolated human secreted proteins.

XX

PS Claim 9; Page 185-186; 516pp; English.

XX

CC This sequence is encoded by an extended human secreted protein coding  
CC sequence of the invention. The secreted proteins can be used in treating  
CC or controlling a variety of human conditions. The secreted proteins may  
CC act as cytokines or may affect cellular proliferation or differentiation  
CC or may act as immune system regulators, haematopoiesis regulators, tissue  
CC growth regulators, regulators of reproductive hormones or cell movement  
CC or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or  
CC tumour inhibition activity. The DNAs can be used in forensic procedures  
CC to identify individuals or in diagnostic procedures to identify  
CC individuals having genetic diseases resulting from abnormal expression of  
CC the genes corresponding to the extended cDNAs. They are also useful for  
CC constructing a high resolution map of the human chromosomes. They can  
CC also be used for gene therapy to control or treat genetic diseases

XX

SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 2; Length 199;  
Best Local Similarity 98.1%; Pred. No. 6.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 7

AAB12805

ID AAB12805 standard; protein; 199 AA.

XX

AC AAB12805;

XX

DT 24-NOV-2000 (first entry)

XX

DE Human NSPH protein sequence SEQ ID NO:4.

XX

KW Human; neuroendocrine-specific protein; NSPH; NSPA; NSPB; NSPC.

XX

OS Homo sapiens.

XX

PN CN1253180-A.

XX

PD 17-MAY-2000.

XX

PF 30-OCT-1998; 98CN-00121473.

XX

PR 30-OCT-1998; 98CN-00121473.

XX

PA (UYFU-) UNIV FUDAN.

XX

PI Yu L, Zhao Y, Zhang H;

XX

DR WPI; 2000-466537/41.

DR N-PSDB; AAA72981.

XX

PT Specific protein of human neuroendocrine, coding sequence and its  
PT preparing process and application.

XX

PS Claim 4; Page 14-15; 21pp; Chinese.

XX

CC The present invention relates to a new member of the human neuroendocrine  
CC specific protein family, designated NSPH. The present sequence represents  
CC the human NSPH protein

XX

SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 3; Length 199;  
Best Local Similarity 98.1%; Pred. No. 6.4e-51;

Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 8

AAB82348

ID AAB82348 standard; protein; 199 AA.

XX

AC AAB82348;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-C protein.

XX

KW NOGO-C; human; chromosome 2p21; neuropathy; spinal injury; brain injury; stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease; neuromuscular disorder; psychiatric disorder; developmental disorder; neuroprotective; nootropic; neuroleptic; antiparkinsonian; cerebroprotective; neuroleptic; diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO200136631-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-GB004345.

XX

PR 15-NOV-1999; 99GB-00026995.

PR 24-JAN-2000; 2000GB-00001550.

XX

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha R;

XX

DR WPI; 2001-343822/36.

DR N-PSDB; AAF90323.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO gene and may be useful in the treatment of neural disorders including Alzheimer's and Parkinson's diseases.

XX

PS Claim 3; Page 25; 25pp; English.

XX

CC The present sequence is that of human NOGO-C, encoded by a novel splice variant of the human NOGO gene on chromosome 2p21. 2 Other splice variants, NOGO-A and NOGO-B, have previously been identified. The invention provides NOGO-C polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also disclosed are methods for utilising NOGO-C polypeptides and polynucleotides in the



XX  
PT Identifying modulators of Nogo or BACE activity for treating acute  
PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
PT providing and monitoring interaction between Nogo and BACE polypeptides.  
XX  
PS Disclosure; Page 64; 68pp; English.  
XX  
CC The present invention relates to a new method of identifying modulators  
CC of Nogo function or BACE activity. The method involves providing Nogo and  
CC BACE polypeptides capable of binding with each other, monitoring the  
CC interaction between these polypeptides, and determining if the test agent  
CC is a modulator of Nogo or BACE activity. The method is useful in treating  
CC acute neuronal injuries, such as spinal or head injury, stroke,  
CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
CC hypertrophy) of the central nervous system. The BACE polypeptide is  
CC useful in screening methods to identify agents that may act as modulators  
CC of BACE activity and in particular agents that may be useful in treating  
CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
CC and the polynucleotide encoding the BACE polypeptide are useful in  
CC manufacturing a medicament for the treatment or prevention of disorders  
CC responsive to the modulation of Nogo activity, in alleviating the  
CC symptoms or improving the condition of a patient suffering from this  
CC disorder, in axon regeneration, or in preventing metastasis or spreading  
CC of a cancer. The polynucleotide may also be an essential component in  
CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
CC techniques. The present amino acid sequence represents the human NogoC  
CC protein of the invention  
XX  
SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 5; Length 199;  
Best Local Similarity 98.1%; Pred. No. 6.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFULLSLTVFSIVSVTAYIALALLSVTIS 97  
|||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFULLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 10  
ABB81080  
ID ABB81080 standard; protein; 199 AA.  
XX  
AC ABB81080;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
DE Human neurotransmitter receptor protein Nogo-C.  
XX  
KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
KW central nervous system; peripheral nervous system; tranquilizer; Nogo;

KW vulnerability; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
KW neurotransmitter receptor; human; receptor.  
XX  
OS Homo sapiens.  
XX  
PN US2002072493-A1.  
XX  
PD 13-JUN-2002.  
XX  
PF 28-JUN-2001; 2001US-00893348.  
XX  
PR 19-MAY-1998; 98IL-00124500.  
PR 21-JUL-1998; 98WO-US014715.  
PR 22-DEC-1998; 98US-00218277.  
PR 19-MAY-1999; 99US-00314161.  
XX  
PA (YEDA ) YEDA RES & DEV CO LTD.  
XX  
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;  
PI Moalem G;  
XX  
DR WPI; 2002-607255/65.  
DR N-PSDB; ABN86601.  
XX  
PT Promoting nerve regeneration and preventing neuronal degeneration in the  
PT central/peripheral nervous system from injury/disease, comprises  
PT administering nervous system-specific activated T cells/antigen, or  
PT analogs/peptides.  
XX  
PS Example; Page 57-58; 93pp; English.  
XX  
CC The invention relates to promoting nerve regeneration or conferring  
CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
CC central/peripheral nervous system (NS). The method involves administering  
CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
CC combinations. The method is useful for promoting nerve regeneration and  
CC preventing neuronal degeneration in central/peripheral nervous system  
CC from injury/disease, where the injury is spinal cord injury, blunt  
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
CC damages caused by surgery such as tumour excision. The disease is not an  
CC autoimmune disease or neoplasm. The disease results in a degenerative  
CC process occurring in either gray or white matter or both. The disease is  
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
CC neuropathies associated with various diseases, including but not limited  
CC to uremia, porphyria, hypoglycemia, Sjögren Larsson syndrome, acute  
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia

CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,  
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
CC disease, or lipoproteinemia. The present sequence represents the human  
CC neurotransmitter receptor protein Nogo-C, an example of NS-specific  
CC antigen

XX

SQ Sequence 199 AA;

Query Match 71.3%; Score 503; DB 5; Length 199;  
Best Local Similarity 98.1%; Pred. No. 6.4e-51;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy 98 FRIYGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 FRIYGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 11

AAY71559

ID AAY71559 standard; protein; 199 AA.

XX

AC AAY71559;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo C/Nogo A proteins derived fragment to construct mutant Nogo-C.

XX

KW Rat; neurite growth inhibitor; Nogo A; Nogo C; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Region 1. .11

FT /note= "Corresponds to residues 40-50 of rat Nogo C  
protein shown in AAY71312"

FT Region 12. .199

FT /note= "Corresponds to residues 975-1162 of rat Nogo A  
protein shown in AAY71310"

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.  
PA (CHEN/) CHEN M S.  
XX  
PI Schwab ME, Chen MS;  
XX  
DR WPI; 2000-400052/34.  
XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX  
PS Example; Page; 122pp; English.  
XX  
CC The patent relates to neurite growth inhibitor Nogo which is free of all  
CC central nervous system (CNS) myelin material with which it is natively  
CC associated. Nogo proteins and fragments displaying neurite growth  
CC inhibitory activity are used in the treatment of neoplastic disease of  
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
CC oligodendrolioma, menangioma, neuroblastoma or retinoblastoma and  
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
CC Therapeutics which promote Nogo activity can be used to treat or prevent  
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
CC used to inhibit production of Nogo protein to induce regeneration of  
CC neurons or to promote structural plasticity of the CNS in disorders where  
CC neurite growth, regeneration or maintenance are deficient or desired. The  
CC animal models can be used in diagnostic and screening methods for  
CC predisposition to disorders and to screen for or test molecules which can  
CC treat or prevent disorders or diseases of the CNS. The present sequence  
CC is derived by fusing two fragments from rat Nogo C and Nogo A proteins.  
CC The fragment is used in the construction of mutant Nogo-C which is  
CC composed of His-tag/T7-tag/Nogo-C N-terminus (11 aa) + Nogo-A sequence aa  
CC 975-1162. Nogo A deletion mutants were used for mapping the inhibitory  
CC sites of Nogo protein. Major inhibitory region was identified in the Nogo  
CC A sequence from amino acids 172-974, particularly amino acids 542-722. In  
CC addition, N-terminal region 1-171 was found to be inhibitory to NIH 3T3  
CC fibroblast spreading. Note: The present sequence is not given in the  
CC specification but is derived from rat Nogo C sequence shown in AAY71312  
CC and Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred  
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.  
CC However, the specification does not include sequences for these SEQ ID  
CC numbers  
XX  
SQ Sequence 199 AA;

Query Match 70.9%; Score 499.5; DB 3; Length 199;  
Best Local Similarity 98.1%; Pred. No. 1.7e-50;  
Matches 103; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 38 MDGQKKHWKDK-VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTI 96  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 1 MDGQKKHWKDKSVV DLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTI 60

Qy 97 SFRIYKGVIQAIQAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 61 SFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 105

RESULT 12

AAY71311

ID AAY71311 standard; protein; 1178 AA.

XX

AC AAY71311;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human neurite growth inhibitor Nogo.

XX

KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 187

/label= Unknown

FT Misc-difference 188

/label= Unknown

FT Misc-difference 189

/label= Unknown

FT Misc-difference 190

/label= Unknown

FT Misc-difference 221

/label= Unknown

FT Misc-difference 328

/label= Unknown

FT Misc-difference 477

/label= Unknown

FT Region 977. .1012

/note= "Region specifically described in claim 16"

FT Region 994. .1174

/note= "Region specifically described in claim 16"

FT Region 1079. .1114

/note= "Region specifically described in claim 16"

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX  
PS Claim 11; Fig 13; 122pp; English.  
XX  
CC The present sequence is a human Nogo protein which is a potent neural  
CC cell growth inhibitor and is free of all central nervous system (CNS)  
CC myelin material with which it is natively associated. The human Nogo  
CC sequence was derived by aligning human expressed sequence tags (ESTs)  
CC e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565, AA081525  
CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments  
CC displaying neurite growth inhibitory activity are used in the treatment  
CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
CC haemangioblastoma, acoustic neuroma, oligodendrogloma, menangioma,  
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.  
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
CC activity can be used to treat or prevent hyperproliferative or benign  
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
CC production of Nogo protein to induce regeneration of neurons or to  
CC promote structural plasticity of the CNS in disorders where neurite  
CC growth, regeneration or maintenance are deficient or desired. The animal  
CC models can be used in diagnostic and screening methods for predisposition  
CC to disorders and to screen for or test molecules which can treat or  
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However the specification does not include sequences for  
CC these SEQ ID numbers  
XX  
SQ Sequence 1178 AA;

Query Match 63.5%; Score 448; DB 3; Length 1178;  
Best Local Similarity 74.6%; Pred. No. 2.2e-43;  
Matches 97; Conservative 3; Mismatches 8; Indels 22; Gaps 1;

Qy 12 RENFAVYSVSVMHNLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFL 71  
| ::| :| | ||||||| ||||| ||||| ||||| |||||  
Db 976 RSPSAIFSAIDLG-----KTSVVDLLYWRDIKKTGVVFGASLFL 1013

Qy 72 LLSLTIVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEEL 131  
| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1014 LLSLTIVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLESEVAISEEL 1073

Qy 132 VQKYSNSALG 141  
| |||||  
Db 1074 VQKYSNSALG 1083

RESULT 13  
AAY71563  
ID AAY71563 standard; protein; 403 AA.  
XX  
AC AAY71563;  
XX  
DT 02-NOV-2000 (first entry)

XX  
DE Rat Nogo A protein fragment used in the construction of mutant EST.  
XX  
KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
KW central nervous system; neoplastic disease; antiproliferative; glioma;  
KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;  
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
KW structural plasticity; screening; mutant; mutein.  
XX  
OS Rattus sp.  
XX  
PN WO200031235-A2.  
XX  
PD 02-JUN-2000.  
XX  
PF 05-NOV-1999; 99WO-US026160.  
XX  
PR 06-NOV-1998; 98US-0107446P.  
XX  
PA (SCHW/) SCHWAB M E.  
PA (CHEN/) CHEN M S.  
XX  
PI Schwab ME, Chen MS;  
XX  
DR WPI; 2000-400052/34.  
XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX  
PS Example; Page; 122pp; English.  
XX  
CC The patent relates to neurite growth inhibitor Nogo which is free of all  
CC central nervous system (CNS) myelin material with which it is natively  
CC associated. Nogo proteins and fragments displaying neurite growth  
CC inhibitory activity are used in the treatment of neoplastic disease of  
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
CC oligodendrogloma, menangioma, neuroblastoma or retinoblastoma and  
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
CC Therapeutics which promote Nogo activity can be used to treat or prevent  
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
CC used to inhibit production of Nogo protein to induce regeneration of  
CC neurons or to promote structural plasticity of the CNS in disorders where  
CC neurite growth, regeneration or maintenance are deficient or desired. The  
CC animal models can be used in diagnostic and screening methods for  
CC predisposition to disorders and to screen for or test molecules which can  
CC treat or prevent disorders or diseases of the CNS. The present sequence  
CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in  
CC the construction of mutant EST. The mutant is composed of His-tag/T7-  
CC tag/Nogo-A sequence aa 760-1162. Nogo A deletion mutants were used for  
CC mapping the inhibitory sites of Nogo protein. Major inhibitory region was  
CC identified in the Nogo A sequence from amino acids 172-974, particularly  
CC amino acids 542-722. In addition, N-terminal region 1-171 was found to be  
CC inhibitory to NIH 3T3 fibroblast spreading. Note: The present sequence is



XX  
PT New secreted or transmembrane proteins and polynucleotides encoding them,  
PT useful for treating neurodegenerative disorders, autoimmune diseases and  
PT cancer.  
XX  
PS Claim 73; Page 322-325; 357pp; English.  
XX  
CC The invention relates to 40 human secreted proteins (AAV94981-Y95020),  
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins  
CC of the invention include those that are thought to be only partially  
CC secreted, i.e., transmembrane proteins. The proteins of the invention may  
CC exhibit one or more activities selected from the following: cytokine  
CC activity; cell proliferation; differentiation; immune modulation;  
CC haematopoiesis regulation; tissue growth activity; activin/inhibin  
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic  
CC activity; anti-inflammatory activity; and tumour inhibition activity. The  
CC proteins may be administered to patients as vaccines, and the nucleotides  
CC may be used as part of a gene therapy regime. Diseases or conditions that  
CC may be treated using the proteins or nucleotides of the invention include  
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular  
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;  
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;  
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and  
CC allergic reactions such as asthma and anaemia. They may also be used for  
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal  
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease  
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin  
CC activity may additionally be useful as contraceptives. Nucleic acid  
CC sequences of the invention may be used in chromosome mapping, and as a  
CC source of diagnostic primers and probes. The present sequence represents  
CC one of the 40 proteins of the invention  
XX  
SQ Sequence 893 AA;

```

Query Match           63.4%; Score 447; DB 3; Length 893;
Best Local Similarity 96.9%; Pred. No. 2e-43;
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105
        |   ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      703 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 762

Qy      106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
        ||| | | | | | | | | | | | | | | | | | | | | |
Db      763 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 798

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RESULT 15  
ABU11573  
ID ABU11573 standard; protein; 983 AA  
XX  
AC ABU11573;  
XX  
DT 12-FEB-2003 (first entry)  
XX  
DE Human MDDT polypeptide SEQ ID 520.  
XX

KW MDDT; human; disease detection and treatment molecule polypeptide;  
KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;  
KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;  
KW gene therapy; protein replacement therapy; cell proliferative disorder;  
KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
KW psoriasis; hepatitis.  
XX  
OS Homo sapiens.  
XX  
PN WO200279449-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 27-MAR-2002; 2002WO-US009944.  
XX  
PR 28-MAR-2001; 2001US-0279619P.  
PR 29-MAR-2001; 2001US-0280067P.  
PR 29-MAR-2001; 2001US-0280068P.  
PR 16-MAY-2001; 2001US-0291280P.  
PR 17-MAY-2001; 2001US-0291829P.  
PR 17-MAY-2001; 2001US-0291849P.  
PR 19-JUN-2001; 2001US-0299428P.  
PR 20-JUN-2001; 2001US-0299776P.  
PR 20-JUN-2001; 2001US-0300001P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
XX  
DR WPI; 2003-058431/05.  
DR N-PSDB; ABX34563.  
XX  
PT New purified disease detection and treatment molecule proteins and  
PT polynucleotides, useful for diagnosing, treating or preventing cancers  
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis  
PT or hepatitis.  
XX  
PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.  
XX  
CC This invention describes a novel disease detection and treatment molecule  
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,  
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides  
CC and the polypeptides of the invention can be used for gene therapy,  
CC protein replacement therapy and are useful for treating a variety of  
CC diseases or conditions. These polypeptides or polynucleotides are  
CC particularly useful for diagnosing, treating or preventing cell  
CC proliferative disorders (e.g. cancers including adenocarcinoma,  
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or

CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded  
CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format from WIPO at  
CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences)  
XX

SQ Sequence 983 AA;

Query Match 63.4%; Score 447; DB 6; Length 983;  
Best Local Similarity 96.9%; Pred. No. 2.3e-43;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 793 KTSVVDLLYWRDIKKTGVVF GASLFL LSLTVFSIVS VTAYIAL ALLSVT ISFRI YKGVI 852

Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141

11 256

Search completed: September 29, 2004, 18:14:02

Job time : 13.3745 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:09:33 ; Search time 3.50035 Seconds  
(without alignments)  
2079.581 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB	
1	503	71.3	199	2	US-08-700-607-1 Sequence 1, Appli
2	349	49.5	208	2	US-08-700-607-7 Sequence 7, Appli
3	348	49.4	267	2	US-08-700-607-8 Sequence 8, Appli
4	337	47.8	356	2	US-08-700-607-6 Sequence 6, Appli
5	337	47.8	776	2	US-08-700-607-5 Sequence 5, Appli
6	305	43.3	241	2	US-08-700-607-3 Sequence 3, Appli
7	227	32.2	168	4	US-09-149-476-563 Sequence 563, App
8	99	14.0	80	3	US-08-905-223-411 Sequence 411, App
9	75	10.6	593	4	US-09-328-352-4866 Sequence 4866, Ap
10	72.5	10.3	598	2	US-08-853-659A-53 Sequence 53, Appli
11	71.5	10.1	154	1	US-08-366-783-5 Sequence 5, Appli

12	70	9.9	518	4	US-09-134-001C-4744	Sequence 4744, Ap
13	70	9.9	563	4	US-09-422-936-79	Sequence 79, Appl
14	70	9.9	619	3	US-08-262-220-6	Sequence 6, Appl
15	70	9.9	619	3	US-08-471-733-6	Sequence 6, Appl
16	70	9.9	619	3	US-08-468-878-6	Sequence 6, Appl
17	70	9.9	619	3	US-08-750-494-6	Sequence 6, Appl
18	70	9.9	619	4	US-08-470-638-6	Sequence 6, Appl
19	70	9.9	844	4	US-09-422-936-47	Sequence 47, Appl
20	70	9.9	844	4	US-09-422-936-51	Sequence 51, Appl
21	70	9.9	886	4	US-09-422-936-77	Sequence 77, Appl
22	70	9.9	892	4	US-09-422-936-75	Sequence 75, Appl
23	70	9.9	899	4	US-09-422-936-71	Sequence 71, Appl
24	70	9.9	960	4	US-09-422-936-45	Sequence 45, Appl
25	70	9.9	961	4	US-09-422-936-49	Sequence 49, Appl
26	70	9.9	961	4	US-09-914-259-14	Sequence 14, Appl
27	69	9.8	621	3	US-08-262-220-8	Sequence 8, Appl
28	69	9.8	621	3	US-08-471-733-8	Sequence 8, Appl
29	69	9.8	621	3	US-08-468-878-8	Sequence 8, Appl
30	69	9.8	621	3	US-08-750-494-8	Sequence 8, Appl
31	69	9.8	621	4	US-08-470-638-8	Sequence 8, Appl
32	68	9.6	344	4	US-09-107-532A-6886	Sequence 6886, Ap
33	68	9.6	1447	3	US-09-041-886-25	Sequence 25, Appl
34	68	9.6	1447	5	PCT-US94-05277-2	Sequence 2, Appl
35	67.5	9.6	659	4	US-09-328-352-6021	Sequence 6021, Ap
36	67	9.5	231	4	US-09-198-452A-419	Sequence 419, App
37	67	9.5	493	4	US-09-540-236-2120	Sequence 2120, Ap
38	67	9.5	507	4	US-09-328-352-7742	Sequence 7742, Ap
39	66.5	9.4	249	4	US-09-107-532A-6706	Sequence 6706, Ap
40	66	9.4	445	4	US-09-328-352-4714	Sequence 4714, Ap
41	65.5	9.3	187	2	US-08-846-021A-5	Sequence 5, Appli
42	65.5	9.3	234	1	US-08-366-783-4	Sequence 4, Appli
43	65.5	9.3	254	2	US-08-767-026-7	Sequence 7, Appli
44	65.5	9.3	254	4	US-09-319-275A-7	Sequence 7, Appli
45	65	9.2	424	4	US-09-543-681A-7510	Sequence 7510, Ap

#### ALIGNMENTS

#### RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 199 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE: Consensus

US-08-700-607-1

Query Match 71.3%; Score 503; DB 2; Length 199;  
Best Local Similarity 98.1%; Pred. No. 2.9e-52;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS	97
	:	
Db	1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS	60
Qy	98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG	141
Db	61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG	104

RESULT 2

US-08-700-607-7

; Sequence 7, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.

; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 208 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307311

US-08-700-607-7

Query Match 49.5%; Score 349; DB 2; Length 208;  
Best Local Similarity 63.4%; Pred. No. 8.6e-34;  
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

Qy	37 EMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTI 96
	:   :   : :      :  :  :              :     :
Db	9 KMDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLFFFSLTQFSVVSVVAYLALAALSATI 68
Qy	97 SFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
	:  :   :      :      : :  :  :   :
Db	69 SFRIYKSVLQAVQKTDEGHPKAYLELEITLSQEIQIQQYTD 109

RESULT 3

US-08-700-607-8

; Sequence 8, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA

; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 281046  
US-08-700-607-8

Query Match 49.4%; Score 348; DB 2; Length 267;  
Best Local Similarity 64.0%; Pred. No. 1.6e-33;  
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy	38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFL <del>LLS</del> LT <del>V</del> F <del>S</del> I <del>S</del> VTAYIALALLSVTIS 97
	:   : :      :  :  :            :      :
Db	1 MDCVWSNWKSQAIDLLYWRDIKQTGIVFGSF <del>LLL</del> FSLTQFSVVSVVAYI <del>L</del> AALSATIS 60
Qy	98 FRIYKGVIQAIAKSDEGH <del>P</del> FRAYLESEVAISEELVQKYSN 137
	:  :  :    :    :     : :    :    :
Db	61 FRIYKSVLQAVQKTDEGH <del>P</del> FKAYLEITLSQE <del>Q</del> IQKYTD 100

RESULT 4

US-08-700-607-6  
; Sequence 6, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto

; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 356 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307309  
US-08-700-607-6

Query Match 47.8%; Score 337; DB 2; Length 356;  
Best Local Similarity 67.4%; Pred. No. 5e-32;  
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| | :|||||||:|||:|||:| ||| ||| ||:||| |||:||| ||| ||| ||| ||| |:  
Db 166 KQKAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 225  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137  
||: |:|||||:||| |: :||:| :|||:  
Db 226 QAVQKTDEGHPKAYLEITLSQEIQIQQYTD 257

## RESULT 5

US-08-700-607-5

; Sequence 5, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive

; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 776 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 307307

US-08-700-607-5

Query Match 47.8%; Score 337; DB 2; Length 776;  
Best Local Similarity 67.4%; Pred. No. 1.5e-31;  
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| | :|||||||:|||:|||: | ||| ||| ||:||| |||:||| |||:||| |||:||| |||:||| |||:  
Db 586 KQKAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 645

Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137  
| | :|:|||||:||| |: :|:| :|||:  
Db 646 QAVQKTDEGHPKAYLEITLSQEIQKYTD 677

RESULT 6

US-08-700-607-3

; Sequence 3, Application US/08700607  
; Patent No. 5858708  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/700,607  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 241 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: THP1NOB01  
; CLONE: 31870  
US-08-700-607-3

Query Match 43.3%; Score 305; DB 2; Length 241;  
Best Local Similarity 60.9%; Pred. No. 2e-28;  
Matches 56; Conservative 17; Mismatches 19; Indels 0; Gaps 0;  
  
Qy 49 VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108  
| ||: ||||:|||| ||| :| :|||| ||::|| :|: ||||||||||||| ||||:  
Db 48 VHDLIXWRDVKKTGFGTTLIMLLSAAFSVISVVSYLILALLSVTISFRIYKSVIQA 107  
  
Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140  
||:|||||:|||: :: :|| | | :|:  
Db 108 QKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139

RESULT 7  
US-09-149-476-563  
; Sequence 563, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601

; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,589  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,593  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,614  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,578  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,576  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/047,501  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,670  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/056,632  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,664  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,876  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,881  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,909  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,875

; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,862  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,887  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,908  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/057,650  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/056,884  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,669  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/049,610  
; EARLIER FILING DATE: 1997-06-13  
; EARLIER APPLICATION NUMBER: 60/061,060  
; EARLIER FILING DATE: 1997-10-02

Query Match 32.2%; Score 227; DB 4; Length 168;  
Best Local Similarity 60.0%; Pred. No. 2.7e-19;  
Matches 42; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 71 LLSSLTVEFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEE 130  
:||||| ||::|| :|: ||||||||||||| ||||: ||:|||||:|||: :: :|||  
Db 1 MLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQAQKSEEGHPFKAYLDVDITLSSE 60  
  
Qy 131 LVQKYSNSAL 140  
| |::|:  
Db 61 AFHNYMNAAM 70

RESULT 8

US-08-905-223-411

; Sequence 411, Application US/08905223

; Patent No. 6222029

; GENERAL INFORMATION:

; APPLICANT: Edwards, Jean-Baptiste D.

; APPLICANT: Duelert, Aymeric

; APPLICANT: Lacroix, Bruno

; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS

; NUMBER OF SEQUENCES: 503

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear

; STREET: 501 West Broadway

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-3505

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Win95

; SOFTWARE: Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/905,223

FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 411:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: -78..-1  
IDENTIFICATION METHOD: Von Heijne matrix  
OTHER INFORMATION: score 6.3  
OTHER INFORMATION: seq TLIMLLSWQLSVS/SV

US-08-905-223-411

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Query Match           14.0%;  Score 99;  DB 3;  Length 80;
Best Local Similarity 58.8%;  Pred. No. 0.0002;
Matches   20;  Conservative    7;  Mismatches     5;  Indels      2;  Gaps      1;

W 49 VVDLLYWRDIKKTGVVFGASLFLLLS--LTVFSI 80
| ||::|||:|||| | || :|||  ||| |:
D 47 VHDLIFWRDVKKTGFVFGTTLIMLLSWOLSVSSV 80

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### RESULT 9

US-09-328-352-4866

; Sequence 4866, Application US/09328352

; Patent No. 6562958

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

## **ACINETOBACTER**

; TITLE OF INVENTION: BAUMAN

; FILE REFERENCE: GTC99-03PA CURRENT ADDRESS: 1000 BROADWAY, NEW YORK, NY 10036

; CURRENT APPLICATION NUMBER: US/

; CURRENT FILING DATE: 1999-0  
NUMBER OF SEC ID NO.: 2050

; NUMBER OF SEQ 1  
; SEQ ID NO: 1866

; SEQ ID NO 486  
; LENGTH: 503

TYPE: RBT

ORGANISM: *Acinetobacter baumannii*

US-09-328-352-4866

Query Match 10.6% Score 75 DB 4 Length 593

Best Local Similarity 27.5%: Pred No 25:

Matches 25; Conservative 19; Mismatches 27; Indels 20; Gaps 5;

```

Qy      55 WRDIKKT--GVVFGASLFLLLSLTVFSIV-----SVTAYIALALLSVTISFRIYKGVIA 107
       || :|:| |: | | : : :|| || :|:|: ||::|
Db      258 WRGVKETWPAVLVGGGAFIAQYLTNSFIGPELPDITAAIA-SLVSLLFRVWK----- 311

Qy      108 IAKSDEGHPFRAYLESEVAISEE--LVQKYS 136
       | || |: :::: ||:|| |
Db      -----PKHIFRFEPEAGQTLAQQPPTTVQRYS 337

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RESULT 10

US-08-853-659A-53

```

; Sequence 53, Application US/08853659A
; Patent No. 5925522
; GENERAL INFORMATION:
;   APPLICANT: Wong, K.K.; Saffer, J.D.
;   TITLE OF INVENTION: A Salmonella Sequence, Methods Of Detection
;   TITLE OF INVENTION: Of A
;   TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of
Salmonella
;   NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Paul W. Zimmerman
;   ADDRESSEE: Intellectual Property Services
;   ADDRESSEE: Battelle Memorial Institute
;   ADDRESSEE: PNNL P.O. Box 999
;   STREET: Washington Way
;   CITY: Richland
;   STATE: Washington
;   COUNTRY: U.S.A.
;   ZIP: 99352
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
;   COMPUTER: IBM PC/XT/AT
;   OPERATING SYSTEM: MS-DOS
;   SOFTWARE: Word Processor (WordPerfect 5.1)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/853,659A
;   FILING DATE: Unknown
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: none
;   FILING DATE: n/a
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 598 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear

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US-08-853-659A-53

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Query Match          10.3%; Score 72.5; DB 2; Length 598;
Best Local Similarity 22.5%; Pred. No. 5;
Matches 25; Conservative 22; Mismatches 53; Indels 11; Gaps 2;

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Qy      41 QKKHWKDKVVDLLYWRDIKKTGVVFGASLF-LLLSLTVFSIVSVTAYIALAL----- 91
       :||: : : | : :| | | :| : :| | : |: | |
Db      149 KKKNGRSMSSAFVLWNEFQKIKPVLLNSIFQRIADIPIFIIFLIVIYVNGLVVIVPITM 208

```

Qy 92 --LSVTISFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140  
; :|: || : : | || | | || :| ::: :| |  
Db 209 FIVSIIISLVNHHYTNELMNQKEGQKNRNIFISEVFLSIKMIHTLNNQGL 259

RESULT 11

US-08-366-783-5

; Sequence 5, Application US/08366783

; Patent No. 5650554

; GENERAL INFORMATION:

; APPLICANT: Moloney, Maurice M

; TITLE OF INVENTION: Oil-Body Proteins As Carriers Of

; TITLE OF INVENTION: High-Value Peptides In Plants

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DEHLINGER & ASSOCIATES

; STREET: 350 CAMBRIDGE AVENUE, SUITE 250

; CITY: PALO ALTO

; STATE: California

; COUNTRY: United States

; ZIP: 94025-1536

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/366,783

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: FABIAN, GARY

; REGISTRATION NUMBER: 33,875

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-324-0880

; TELEFAX: 415-324-0960

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 154 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-366-783-5

Query Match 10.1%; Score 71.5; DB 1; Length 154;  
Best Local Similarity 26.2%; Pred. No. 1;  
Matches 37; Conservative 16; Mismatches 49; Indels 39; Gaps 5;

Qy 33 RSWQEMDGQKKHWKDKVVDLLYWRDIKK--TGVVFGASLFLLSLT----- 76  
| :| :| : : | | | | | | | | :|||||  
Db 6 RDQYQMSGRGSDYSKS-----RQIAKAATAVTAGGSLLVLLSLLVGTVIALTVATPL 58

Qy 77 --VFSIVSVTAYIALALL-----SVTISFRIYKG-VIQAIAKSDEGHPFRAY 120  
:|| : | | | :||| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Db 59 LVIFSPILVPALITVALLITGFLSSGGFGIAAITVFSWIYKYLLIEHPQGSDKLDSARMK 118

Qy 121 LESEVAISEELVQKYSNSALG 141  
| |: :: | | |  
Db 119 LGSKAQDLKDRAQYYGQQHTG 139

RESULT 12  
US-09-134-001C-4744  
; Sequence 4744, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4744  
; LENGTH: 518  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4744

Query Match 9.9%; Score 70; DB 4; Length 518;  
Best Local Similarity 21.0%; Pred. No. 8.1;  
Matches 21; Conservative 28; Mismatches 35; Indels 16; Gaps 4;

Qy 16 AVYSVSVGGMH---NLLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKK---TGVVFGAS 68  
|: :::: | :|| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Db 400 AIVAITIAWHPNDTILNLVGNAWA---GFGAAFSPLVLYSLYWKDLTRAGAISGMVAGAV 456  
  
Qy 69 LFLLLSLTVFSIVSVTAYIAL-----ALLSVTISFRIYK 102  
: :: : : | : : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Db 457 VVIVWISWIKPLATINAFFGMYEIIIPGFIVSVLITYIVSK 496

RESULT 13  
US-09-422-936-79  
; Sequence 79, Application US/09422936  
; Patent No. 6465213  
; GENERAL INFORMATION:  
; APPLICANT: Ekstrand, Jonas  
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES  
; FILE REFERENCE: 06275-165002  
; CURRENT APPLICATION NUMBER: US/09/422,936  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: US 09/242,608  
; PRIOR FILING DATE: 1999-02-19  
; PRIOR APPLICATION NUMBER: PCT/SE98/01947  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2

: PRIOR FILING DATE: 1997-10-27  
: PRIOR APPLICATION NUMBER: SWEDEN 9800864-2  
: PRIOR FILING DATE: 1998-03-16  
: PRIOR APPLICATION NUMBER: SWEDEN 9802575-2  
: PRIOR FILING DATE: 1998-07-17  
: NUMBER OF SEQ ID NOS: 85  
: SOFTWARE: FastSEQ for Windows Version 4.0  
: SEQ ID NO 79  
: LENGTH: 563  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-422-936-79

Query Match 9.9%; Score 70; DB 4; Length 563;  
Best Local Similarity 28.3%; Pred. No. 9.1;  
Matches 26; Conservative 13; Mismatches 35; Indels 18; Gaps 3;

Qy 30 LEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGAS-----LFLLSLTVFS 79  
| : | | :: : : | | | || | | | | | | : |  
Db 144 LQGGSYKKIG----YYDSTKDDLSW---SKTDKWIGGSPPADQTLVIKTFRFLSQKLFI 195  
  
Qy 80 IVSVTAYIALALLSVTISFRIYKGVIQAIAKS 111  
||| : : : | | : || || :: | |  
Db 196 SVSVLSSLGIVLAVVCLSFNIYNNSHVRYIQNS 227

#### RESULT 14

US-08-262-220-6

: Sequence 6, Application US/08262220  
: Patent No. 6054296  
: GENERAL INFORMATION:  
: APPLICANT: BERGSTROM SVEN  
: APPLICANT: BARBOUR ALAN G.  
: TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA  
: NUMBER OF SEQUENCES: 14  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: BROWDY AND NEIMARK  
: STREET: 419 SEVENTH STREET, N.W.  
: CITY: WASHINGTON  
: COUNTRY: USA  
: ZIP: 20004  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/262,220  
: FILING DATE: 20-JUN-1994  
: CLASSIFICATION: 514  
: ATTORNEY/AGENT INFORMATION:  
: NAME: COOPER, IVER P.  
: REGISTRATION NUMBER: 28,005  
: REFERENCE/DOCKET NUMBER: BERGSTROM=3  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 202-628-5197  
: TELEFAX: 202-737-3528

; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 619 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-262-220-6

Query Match 9.9%; Score 70; DB 3; Length 619;  
Best Local Similarity 39.0%; Pred. No. 10;  
Matches 16; Conservative 6; Mismatches 15; Indels 4; Gaps 1;  
  
Qy 32 GRSWQEMDGQKKHWKDKVVD---LLYWRDIKKTGVVFGAS 68  
| :| :||:|:|| | | |:||:|| || |  
Db 384 GLAWNKDDGEKESWKVGSDSYSTRLFGEQDKKSGVALGIS 424

RESULT 15  
US-08-471-733-6  
; Sequence 6, Application US/08471733  
; Patent No. 6068842  
; GENERAL INFORMATION:  
; APPLICANT: BERGSTROM SVEN  
; APPLICANT: BARBOUR ALAN G.  
; TITLE OF INVENTION: NEW 66 KDA ANTIGEN FROM BORRELIA  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 SEVENTH STREET, N.W.  
; CITY: WASHINGTON  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,733  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/262,220  
; FILING DATE: 20-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, IVER P.  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: BERGSTROM=3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 619 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-471-733-6

Query Match 9.9%; Score 70; DB 3; Length 619;  
Best Local Similarity 39.0%; Pred. No. 10;  
Matches 16; Conservative 6; Mismatches 15; Indels 4; Gaps 1;

Qy 32 GRSWQEMDGQKKHWKDKVVD----LLYWRDIKKTGVVFGAS 68  
| :| :||:|| | | | | | | | | | | | |  
Db 384 GLAWNKKDDGEKESWKVGSDSYSTRLFGEQDKKSGVALGIS 424

Search completed: September 29, 2004, 18:21:06  
Job time : 4.50035 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:05:43 ; Search time 3.45105 Seconds  
(without alignments)  
3930.111 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	349	49.5	208	2	I60904	neuroendocrine-spe
2	348	49.4	267	2	A60021	tropomyosin-relate
3	337	47.8	776	2	A46583	neuroendocrine-spe
4	162	23.0	2484	2	T26216	hypothetical prote
5	159	22.6	2607	2	T26215	hypothetical prote
6	158	22.4	222	2	T26213	hypothetical prote
7	83.5	11.8	295	2	S59439	probable membrane
8	81.5	11.6	464	2	C88188	protein C18H9.5 [i
9	79	11.2	618	2	T24228	hypothetical prote
10	78.5	11.1	458	2	A72258	hypothetical prote
11	77.5	11.0	261	2	F64924	probable thiosulfa
12	77.5	11.0	583	2	T49359	hypothetical prote
13	76.5	10.9	481	2	C95920	hypothetical membr

14	75.5	10.7	545	2	F64665	glucose-6-phosphat
15	74.5	10.6	545	2	E71851	glucose-6-phosphat
16	74	10.5	268	2	F64024	hypothetical prote
17	73	10.4	393	2	S67763	probable membrane
18	73	10.4	888	2	T01081	hypothetical prote
19	72.5	10.3	278	2	AD0147	probable ABC trans
20	72.5	10.3	302	2	AE2863	conserved hypothet
21	72.5	10.3	302	2	D97640	hypothetical prote
22	72.5	10.3	417	2	B96977	probable Mn transp
23	72.5	10.3	598	2	T14886	leukotoxin express
24	72	10.2	271	2	T13013	hypothetical prote
25	72	10.2	299	2	B69155	hypothetical prote
26	72	10.2	1783	2	T42386	unconventional myo
27	72	10.2	3511	2	A59295	unconventional myo
28	71.5	10.1	255	2	E84899	hypothetical prote
29	71.5	10.1	537	2	G82873	conserved hypothet
30	71	10.1	346	1	WMVZ1W	3beta-hydroxy-Delt
31	71	10.1	346	1	WMVZ2W	3beta-hydroxy-Delt
32	71	10.1	346	2	T37430	hydroxysteroid deh
33	71	10.1	476	2	B97096	2-oxoglutarate/mal
34	71	10.1	1065	2	T25068	hypothetical prote
35	70.5	10.0	153	2	AB3226	conserved hypothet
36	70.5	10.0	261	2	A90926	hypothetical prote
37	70.5	10.0	261	2	E85774	hypothetical prote
38	70.5	10.0	291	2	B69098	phosphate transpor
39	70	9.9	271	2	AC1320	hypothetical prote
40	70	9.9	619	2	S55502	membrane-associate
41	70	9.9	737	2	AE1678	heavy metal-transp
42	69.5	9.9	188	2	T04714	hypothetical prote
43	69.5	9.9	403	2	T04821	hypothetical prote
44	69.5	9.9	415	2	D95248	conserved hypothet
45	69.5	9.9	504	2	E83898	spore germination

## ALIGNMENTS

### RESULT 1

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999

C;Accession: I60904

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 49.5%; Score 349; DB 2; Length 208;  
Best Local Similarity 63.4%; Pred. No. 5.3e-28;  
Matches 64; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

Qy	37 EMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTI 96 :   :   : :       :  :  :             :             :
Db	9 KMDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATI 68
Qy	97 SFRIYKGVIQAIKSDLEGHPFRAYLESEVAISEELVQKYSN 137       :  :  :     :      : :  :  :   :
Db	69 SFRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTD 109

### RESULT 2

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.

A;Reference number: A60021; MUID:91278684; PMID:1647480

A;Accession: A60021

A;Molecule type: mRNA

A;Residues: 1-267 <WIE>

A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550

C;Comment: This neuronal-specific mRNA was identified by hybridization to an alpha-tropomyosin probe but does not show homology in amino acid sequence.

Query Match 49.4%; Score 348; DB 2; Length 267;  
Best Local Similarity 64.0%; Pred. No. 8.9e-28;  
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy	38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97    :   : :       :  :  :             :             :
Db	1 MDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATIS 60
Qy	98 FRIYKGVIQAIKSDLEGHPFRAYLESEVAISEELVQKYSN 137       :  :  :     :      : :  :  :   :
Db	61 FRIYKSVLQAVQKTDEGHPFKAYLELEITLSQEIQKYTD 100

### RESULT 3

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 421-776 <ROE2>

A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309

C;Genetics:

A;Gene: GDB:RTN1; NSP

A;Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 47.8%; Score 337; DB 2; Length 776;  
Best Local Similarity 67.4%; Pred. No. 3.7e-26;  
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| | :|||||||:|||:|||: | || ||| ||:||| ||| ||| ||| ||| |:  
Db 586 KQKAIDLLYWRDIKQTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 645

Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137  
||: |:||||||:|||| |: ::| :|||::  
Db 646 QAVQKTDEGHPKAYLEITLSQEIQKYTD 677

#### RESULT 4

T26216

hypothetical protein W06A7.3c - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T26216

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26216

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2484 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB51467.1; GSPDB:GN00023; CESP:W06A7.3c

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3c

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

Query Match 23.0%; Score 162; DB 2; Length 2484;  
Best Local Similarity 31.5%; Pred. No. 7.9e-08;  
Matches 34; Conservative 22; Mismatches 48; Indels 4; Gaps 1;

Qy 25 HNLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVT 84

|::| | :| :| | |:||:|||| ||: :| :| :| | : ::|  
Db 2269 HSILKHHGDAWIDF----KTVPPCVLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVV 2324  
  
Qy 85 AYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELV 132  
| | | | ||::| | | |:| ||| | :: : :| |  
Db 2325 TYSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLQEKV 2372

RESULT 5  
T26215  
hypothetical protein W06A7.3a - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T26215  
R;Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A;Reference number: Z20173  
A;Accession: T26215  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-2607 <WIL>  
A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a  
A;Experimental source: clone W06A7  
C;Genetics:  
A;Gene: CESP:W06A7.3a  
A;Map position: 5  
A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;  
2586/2

Query Match 22.6%; Score 159; DB 2; Length 2607;  
Best Local Similarity 34.5%; Pred. No. 1.7e-07;  
Matches 30; Conservative 19; Mismatches 38; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| :|:|:||| ||: :| :| :| :| :| | | | ||::| |  
Db 2409 KKEVLDVIYWRDAKKSAIVLSLALLVLFVLAKYPLLTVVTSLLLALGAAAGFRVFKKVE 2468  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELV 132  
| :| | ||| | :: : :| |  
Db 2469 AQIKKTDSEHPFSEILAQDLTLQEKV 2495

RESULT 6  
T26213  
hypothetical protein W06A7.3b - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T26213  
R;Ainscough, R.  
submitted to the EMBL Data Library, August 1996  
A;Reference number: Z20173  
A;Accession: T26213  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-222 <WIL>  
A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b  
A;Experimental source: clone W06A7

C;Genetics:  
A;Gene: CESP:W06A7.3b  
A;Map position: 5  
A;Introns: 27/1; 77/2; 201/2

Query Match 22.4%; Score 158; DB 2; Length 222;  
Best Local Similarity 34.1%; Pred. No. 1.4e-08;  
Matches 29; Conservative 19; Mismatches 37; Indels 0; Gaps 0;  
  
Qy 48 KVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 107  
|::|::||| ||: :| :| :| : ::| | | | ||::| |  
Db 26 KILDVIYWRDAKKSATIVLSALLVLFVLAKYPLLTVVTVYSLLLALGAAAGFRVFKVVEAQ 85  
  
Qy 108 IAKSDEGHPFRAYLESEVAISEELV 132  
| |:| ||| | :: : :: | |  
Db 86 IKKTDSEHPFSEILAQDLTLPQEKV 110

RESULT 7  
S59439  
probable membrane protein YDR233c - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: hypothetical protein YD9934.17c  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 30-Nov-1995 #sequence\_revision 16-Feb-1996 #text\_change 19-Apr-2002  
C;Accession: S59439  
R;Murphy, L.; Harris, D.  
submitted to the EMBL Data Library, March 1995  
A;Reference number: S59423  
A;Accession: S59439  
A;Molecule type: DNA  
A;Residues: 1-295 <MUR>  
A;Cross-references: EMBL:Z48612; NID:g728671; PID:g728688; GSPDB:GN00004;  
MIPS:YDR233c  
A;Experimental source: strain AB972  
C;Genetics:  
A;Gene: MIPS:YDR233c  
A;Cross-references: SGD:S0002641  
A;Map position: 4R  
C;Keywords: transmembrane protein  
F;40-56/Domain: transmembrane #status predicted <TM1>  
F;146-162/Domain: transmembrane #status predicted <TM2>

Query Match 11.8%; Score 83.5; DB 2; Length 295;  
Best Local Similarity 26.3%; Pred. No. 0.73;  
Matches 25; Conservative 17; Mismatches 32; Indels 21; Gaps 2;  
  
Qy 41 QKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRI 100  
|::| ||| ||: :|| ||| ||| ||| | :::: :| :| |  
Db 12 QQQQQKSCNC DLLWRNPVQTGKYFGGSLLALLLKKVNLTFFLKVAYTILFTT---- 66  
  
Qy 101 YKGVIQAI AKA KSDEGHPFRAYLESEVAISEELVQKY 135  
| |: :| : : :| :| | |  
Db 67 --GSIEFVSK-----LFLGQGLITKY 85

RESULT 8  
C88188

protein C18H9.5 [imported] - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C;Accession: C88188  
R;anonymous, The *C. elegans* Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode *C. elegans*: a platform for  
investigating biology.  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/*C\_elegans*/ and  
www.sanger.ac.uk/Projects/*C\_elegans*/ for a list of authors  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103,  
1999; and Science 285, 1493, 1999  
A;Accession: C88188  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-464 <STO>  
A;Cross-references: GB:chr\_II; PID:g722384; GSPDB:GN00020; CESP:C18H9.5  
C;Genetics:  
A;Gene: C18H9.5  
A;Map position: 2

```

Query Match           11.6%;  Score 81.5;  DB 2;  Length 464;
Best Local Similarity 25.9%;  Pred. No. 1.9;
Matches   38;  Conservative  28;  Mismatches  50;  Indels   31;  Gaps     8;

Qy      8 VSCLRENFAVYSVSGMHNLLLEGRSWQEMDGQKKHWKDKVVDLLYWRDIKKTGVVFG- 66
       ::|   |  : : : ||  | : ::| :|:  : ||` :|  |:  | :||

Db      41 ITCTNANMILMNFTVICMNDVIIEQKSF---SNQTHWLEKSSDISLTFSAAVGAIFGT 96

Qy      67 ASLFLLS-----LTVFSIVSV--TAYIALA---LLSVTISFRIYKGV-----I 105
       |::|         |||: :|:  |  : ||  |: | |: |:::||  |

Db      97 VPAVTLLISKYGIRKVLTVYGLSAGGTLLMPLAVNYGLIPVLIA-RLFQGVGASILYSSI 155

Qy      106 QAIAKS---DEGHPFRAYLESEVAIS 128
       |::|  :|  | |:| |  ||

Db      156 GTISESWSPINEIGTFVAFLSSAQFOIS 182

```

## RESULT 9

T24228  
hypothetical protein R166.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T24228  
R;Matthews, P.  
submitted to the EMBL Data Library, August 1995  
A;Reference number: Z19859  
A;Accession: T24228  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-618 <WIL>  
A;Cross-references: EMBL:Z50795; PIDN:CAA90663.1; GSPDB:GN00020; CESP:R166.2  
A;Experimental source: clone R166  
C;Genetics:  
A;Gene: CESP:R166.2  
A;Map position: 2

A; Introns: 41/3; 86/3; 118/3; 164/3; 207/3; 554/3

```

Query Match           11.2%; Score 79; DB 2; Length 618;
Best Local Similarity 29.1%; Pred. No. 4.7;
Matches 32; Conservative 22; Mismatches 32; Indels 24; Gaps 6;
Y      51 DLLYWRDIKK-TGVVFGASLF-LLSLTVF-----SIVSVTAYIALAL---- 91
| : : | : |  | : | : || : || || : | || | | : |
D 353 DIQFWNNRKDLVGLSVRSVLNFQSLIVFLYICDNETNTMVKVTVGIGLLIECWKIPKV 412
Y      92 LSVTISFR-IYGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140
| : | : | : | : || : || : | : || | ::: | | || |
D 413 MNVSIDWQNWKFGVIPRLVISDKG---SYVESETKIYDQMAFKYLGWAL 458

```

RESULT 10

A72258

hypothetical protein - *Thermotoga maritima* (strain MSB8)

C; Species: *Thermotoga maritima*

C; Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text change 21-Jul-2000

C:Accession: A72258

R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson, W.C.; Ketchum, K.A.; McDonald, L.; Utterback, T.R.; Malek, J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.; Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Nature 399, 323–329, 1999

**A;Title:** Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*.

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: A72258

A: Status: preliminary

A: Molecule type: DNA

A;Residues: 1-458 <ARN>  
A;Cross-references: GB:AE001793; GB:AE000512; NID:q4981963; PIDN:AAD36479.1;

PID:q4981972; TIGR:TM1408

## A: Experiment

## C; Genetics:

```

Query Match           11.1%; Score 78.5; DB 2; Length 458;
Best Local Similarity 26.6%; Pred. No. 3.8;
Matches 42; Conservative 17; Mismatches 34; Indels 65; Gaps 9;

y      14 NFAVY-----SVSVGVMHNLLLLEGRSWQEMDGQKKH-----WKD 47
       || : |: :| ||| :|| | |
b     196 NFLILSYLRSSIRIGFDLLL-----TRKHPQLLFIGYFYYLSIWIDNFIAWKV 244

y      48 KVVDLL-----YWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFR 99
       | ::: | | | | | |||| : || ||: | | : | |
b     245 KGIEIAPGFFMSPEY--DIPK---FMASLFFIPSLVVFN-----LSMETVFQR 287

y      100 IYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137
       |||::|:| | ||: | | | : | : | | :|| |
b     288 NYKGLMOSIV-SDK--PMRVISENLLKKLSSLRHAFSN 322

```

RESULT 11  
F64924  
probable thiosulfate-dithiol sulfurtransferase (EC 2.8.1.5) - Escherichia coli  
(strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 03-Jun-2002  
C;Accession: F64924  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;  
Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor,  
J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: F64924  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-261 <BLAT>  
A;Cross-references: GB:AE000262; GB:U00096; NID:g1787955; PIDN: AAC74740.1;  
PID:g1787959; UWGP:b1670  
A;Experimental source: strain K-12, substrain MG1655  
C;Superfamily: hyaC protein  
C;Keywords: sulfurtransferase; transmembrane protein  
F;30-46/Domain: transmembrane #status predicted <TM01>  
F;83-99/Domain: transmembrane #status predicted <TM02>  
F;112-128/Domain: transmembrane #status predicted <TM03>  
F;187-203/Domain: transmembrane #status predicted <TM04>  
F;224-240/Domain: transmembrane #status predicted <TM05>

Query Match 11.0%; Score 77.5; DB 2; Length 261;  
Best Local Similarity 27.6%; Pred. No. 2.6;  
Matches 29; Conservative 16; Mismatches 43; Indels 17; Gaps 4;

Qy	22 VGMHNLLLLEGRSWQEMD-GQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL---SLT 76
	: :            :  :        :  :        :  :
Db	44 LGLHALLRARGVKKSATDHGEKIYLYSKAVRLWHWSN-----ALLFVLLLASGLIN 94

  

Qy	77 VFSIVSVTAYIALALLSVTISFRI---YKGVIQAIAKSDEGHPFR 118
	: :      :  :  :  :  :  :        :
Db	95 HFAMVGATAVKSLVAVHEVCGFLLLACWLGFVLINAVGDNGHHYR 139

RESULT 12  
T49359  
hypothetical protein B1D1.130 [imported] - Neurospora crassa  
C;Species: Neurospora crassa  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C;Accession: T49359  
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.;  
Nyakatura, G.; Mewes, H.W.; Mannhaupt, G.  
submitted to the Protein Sequence Database, May 2000  
A;Reference number: Z25022  
A;Accession: T49359  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-583 <SCH>  
A;Cross-references: EMBL:AL355927; GSPDB:GN00116; NCSP:B1D1.130

A;Experimental source: BAC clone B1D1; strain OR74A

C;Genetics:

A;Gene: NCSP:B1D1.130

A;Map position: 6

A;Introns: 44/1

Query Match 11.0%; Score 77.5; DB 2; Length 583;  
Best Local Similarity 27.5%; Pred. No. 6.2;  
Matches 28; Conservative 13; Mismatches 28; Indels 33; Gaps 4;

Qy 52 LLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKS 111  
| || :: : | | | || | : | . | : || : | | : | :

Db 67 LCYW-PLERRLLVLHALLLSSLEHYS----AYTRVLLLHITSSLNL----- 109

Qy 112 DEGHPFRAYLESEVAIS-----EELVQKYNSNSALG 141  
| | :: | | :: || | : | | | |

Db 110 ----PLRVLVDDEVRAKAIAMAKDINPEELIQKRIEECAG 147

RESULT 13

C95920

hypothetical membrane protein [imported] - *Sinorhizobium meliloti* (strain 1021)  
magaplasmid pSymB

C;Species: *Sinorhizobium meliloti*

C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001

C;Accession: C95920

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernandez-Lucas, I.; Becker, A.; Cowie, A.; Gouzy, J.; Golding, B.; Puhler, A.

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont *Sinorhizobium meliloti*.

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: C95920

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-481 <KUR>

A;Cross-references: GB:AL591985; PIDN:CAC49027.1; PID:g15140512; GSPDB:GN00167

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Barnett, M.J.; Becker, A.; Boistard, P.; Bothe, G.; Boutry, M.; Bowser, L.; Buhrmester, J.; Cadieu, E.; Capela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Gloux, S.; Godrie, T.; Goffeau, A.; Golding, B.; Gouzy, J.; Gurjal, M.; Hernandez-Lucas, I.; Hong, A.; Huizar, L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, V.; Masuy, D.; Palm, C.; Peck, M.C.; Pohl, T.M.; Portetelle, D.; Purnelle, B.; Ramsperger, U.; Surzycki, R.; Thebault, P.; Vandebol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; Batut, J.

A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: SMb21048

A;Genome: plasmid

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Query Match          10.9%;  Score 76.5;  DB 2;  Length 481;
Best Local Similarity 37.7%;  Pred. No. 6.4;
Matches   23;  Conservative   8;  Mismatches   27;  Indels      3;  Gaps      2;

Qy      53 LYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSD 112
       :|||| | | | | ||||| | : | || ||: ||:||: :: | : | : |
Db      238 VYWRKTCSR--VAQALAFLLLVLVLLSTSSV-AYVGLAVLSIPVALSISWSFLSGRMDKD 294

Qy      113 E 113
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Db      295 E 295

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## RESULT 14

F64665  
glucose-6-phosphate isomerase (EC 5.3.1.9) - *Helicobacter pylori* (strain 26695)  
C;Species: *Helicobacter pylori*  
C;Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 16-Jul-1999  
C;Accession: F64665  
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.;  
Fleischmann, R.D.; Ketchum, K.A.; Klenk, H.P.; Gill, S.; Dougherty, B.A.;  
Nelson, K.; Quackenbush, J.; Zhou, L.; Kirkness, E.F.; Peterson, S.; Loftus, B.;  
Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, K.; Fitzgerald,  
L.M.; Lee, N.; Adams, M.D.; Hickey, E.K.; Berg, D.E.; Gocayne, J.D.; Utterback,  
T.R.; Peterson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.;  
Bowman, C.; Watthey, L.  
Nature 388, 539-547, 1997  
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.;  
Fraser, C.M.; Venter, J.C.  
A;Title: The complete genome sequence of the gastric pathogen *Helicobacter*  
*pylori*.  
A;Reference number: A64520; MUID:97394467; PMID:9252185  
A;Accession: F64665  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-545 <TOM>  
A;Cross-references: GB:AE000622; GB:AE000511; NID:g2314317; PIDN:AAD08211.1;  
PID:g2314323; TIGR:HP1166  
C;Superfamily: glucose-6-phosphate isomerase  
C;Keywords: intramolecular oxidoreductase; isomerase

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Query Match           10.7%; Score 75.5; DB 2; Length 545;
Best Local Similarity 25.3%; Pred. No. 9.2;
Matches 37; Conservative 20; Mismatches 44; Indels 45; Gaps 6;

Qy      23 GMHNLL-----LLEGRSWQEMDGQ--KKHWKDKVVDLLYWRDIKKTGVVF GASL 69
        | | :| ::|:|::| |:| | ||:|| :| | | |
Db      411 GHHEILFSNVLAQQAQAFMKGKSYEEALGELLFKGLDKDEAKDLAHHR-----VFFGNRP 464

Qy      70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSD----- 112
        :| | | :| :|| | : :|| | | | | |
Db      465 SNILLLEKISPSNIGALVALYEHKVVF----QGVIWDINSFDQWGVELGKELAVPILQE 519

Qy      113 -EGHPFRAYLESEVAISEELVQKYSN 137
        ||| | | :| ::|:| | |
Db      520 LEGHKSNAYFDSS---TKHLIELYKN 542

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RESULT 15

E71851

glucose-6-phosphate isomerase - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 16-Jul-1999

C;Accession: E71851

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deJonge, B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.; Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Trust, T.J.

Nature 397, 176-180, 1999

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.

A;Reference number: A71800; MUID:99120557; PMID:9923682

A;Accession: E71851

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-545 <ARN>

A;Cross-references: GB:AE001536; GB:AE001439; NID:g4155675; PIDN:AAD06664.1; PID:g4155679

A;Experimental source: strain J99

C;Genetics:

A;Gene: pgi

C;Superfamily: glucose-6-phosphate isomerase

Query Match 10.6%; Score 74.5; DB 2; Length 545;  
Best Local Similarity 25.3%; Pred. No. 12;  
Matches 37; Conservative 19; Mismatches 45; Indels 45; Gaps 6;

Qy 23 GMHNLL-----LLEGRSWQEMDGQ---KKHWKDKVVDLLYWRDIKKTGVVFGASL 69  
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Db 411 GHHEILFSNVLAQAAQAFMKGKSYEEALGELLSKGLDKDEAKDLAHR-----VFFGNRP 464

Qy 70 FLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSD----- 112  
:| | | :| ::|:|| | : :|| | | |  
Db 465 SNILLKEKISPSNIGALVALYEHKVFV----QGVIWDINSFDQWGVELGKELAVPILQE 519

Qy 113 -EGHPFRAYLESEVAISEELVQKYSN 137  
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Db 520 LEGHKSNAFDSS--TRHLIELYKN 542

Search completed: September 29, 2004, 18:16:07

Job time : 5.45105 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:16:15 ; Search time 15.1353 Seconds  
(without alignments)  
2997.869 Million cell updates/sec

Title: US-09-830-972-32  
Perfect score: 705  
Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*

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16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result      Query

No.	Score	Match Length	DB	ID	Description
1	510	72.3	199	9 US-09-893-348-21	Sequence 21, Appl
2	503	71.3	118	15 US-10-264-237-1568	Sequence 1568, Ap
3	503	71.3	199	9 US-09-893-348-25	Sequence 25, Appl
4	503	71.3	199	12 US-10-660-946-1	Sequence 1, Appli
5	503	71.3	199	12 US-09-978-360A-467	Sequence 467, App
6	503	71.3	199	16 US-10-466-258-11	Sequence 11, Appl
7	496	70.4	199	12 US-10-408-967-9	Sequence 9, Appli
8	447	63.4	1163	9 US-09-893-348-18	Sequence 18, Appl
9	447	63.4	1192	9 US-09-789-386-2	Sequence 2, Appli
10	447	63.4	1192	9 US-09-758-140-6	Sequence 6, Appli
11	447	63.4	1192	9 US-09-893-348-23	Sequence 23, Appl
12	447	63.4	1192	9 US-09-972-599A-6	Sequence 6, Appli
13	447	63.4	1192	12 US-10-267-502-429	Sequence 429, App
14	447	63.4	1192	14 US-10-060-036-71	Sequence 71, Appl
15	447	63.4	1192	16 US-10-327-213-9	Sequence 9, Appli
16	447	63.4	1192	16 US-10-466-258-9	Sequence 9, Appli
17	443	62.8	360	9 US-09-893-348-20	Sequence 20, Appl
18	443	62.8	373	9 US-09-789-386-6	Sequence 6, Appli
19	443	62.8	373	9 US-09-765-205-6	Sequence 6, Appli
20	443	62.8	373	9 US-09-893-348-24	Sequence 24, Appl
21	443	62.8	373	12 US-10-408-967-8	Sequence 8, Appli
22	443	62.8	373	14 US-10-060-036-72	Sequence 72, Appl
23	443	62.8	373	16 US-10-466-258-4	Sequence 4, Appli
24	443	62.8	379	14 US-10-205-194-164	Sequence 164, App
25	440	62.4	1192	12 US-10-408-967-7	Sequence 7, Appli
26	436.5	61.9	1163	12 US-10-267-502-431	Sequence 431, App
27	349	49.5	208	12 US-10-660-946-7	Sequence 7, Appli
28	348	49.4	267	12 US-10-660-946-8	Sequence 8, Appli
29	348	49.4	267	14 US-10-205-194-127	Sequence 127, App
30	337	47.8	356	12 US-10-660-946-6	Sequence 6, Appli
31	337	47.8	776	12 US-10-660-946-5	Sequence 5, Appli
32	337	47.8	776	12 US-10-267-502-430	Sequence 430, App
33	337	47.8	777	14 US-10-205-219-93	Sequence 93, Appli
34	337	47.8	780	12 US-10-267-502-432	Sequence 432, App
35	309	43.8	236	9 US-09-729-674-20	Sequence 20, Appl
36	309	43.8	236	9 US-09-765-205-26	Sequence 26, Appl
37	309	43.8	236	12 US-10-408-967-2	Sequence 2, Appli
38	309	43.8	266	12 US-10-276-774-2330	Sequence 2330, Ap
39	309	43.8	269	14 US-10-106-698-6222	Sequence 6222, Ap
40	305	43.3	241	12 US-10-660-946-3	Sequence 3, Appli
41	304	43.1	593	15 US-10-108-260A-2892	Sequence 2892, Ap
42	269	38.2	161	9 US-09-925-302-808	Sequence 808, App
43	269	38.2	161	12 US-09-925-302-808	Sequence 808, App
44	259.5	36.8	204	12 US-10-424-599-194160	Sequence 194160,
45	256	36.3	234	12 US-10-424-599-200840	Sequence 200840,

## ALIGNMENTS

RESULT 1  
US-09-893-348-21  
; Sequence 21, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:

; APPLICANT: EISENBACK-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND  
THEIR USES  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-893-348-21

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Query Match           72.3%; Score 510; DB 9; Length 199;
Best Local Similarity 99.0%; Pred. No. 5.9e-51;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97
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Db      1 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Qy      98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141
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Db      61 FRIYKGVIQAIOKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

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## RESULT 2

US-10-264-237-156

; Sequence 1568, Application US/1026423

; Publication No. US20040009491A1

**GENERAL INFORMATION:**

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA131P1

: CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/1645

PTR OR FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US 60/205,515

: PBTOR FILING DATE: 2000-05

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PatentIn Ver. 3.1

SEQ ID NO 1568

; LENGTH: 118

• 100 •

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (118)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-237-1568

Query Match 71.3%; Score 503; DB 15; Length 118;  
Best Local Similarity 98.1%; Pred. No. 1.9e-50;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	38	MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS	97
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		:	
Qy	98	FRIYKGVIQAIQAKSDEGHPFRAYLESEVAISEELVQKYSNSALG	141
Db	61	FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG	104

RESULT 3

US-09-893-348-25

; Sequence 25, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACK-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND  
THEIR USES  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 199  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-893-348-25

Query Match 71.3%; Score 503; DB 9; Length 199;  
Best Local Similarity 98.1%; Pred. No. 3.9e-50;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
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Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
  
QY 98 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
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Db 61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 4

US-10-660-946-1

; Sequence 1, Application US/10660946

; Publication No. US20040063131A1

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga  
; Au-Young, Janice  
; Goli, Surya K.  
; Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/660,946  
; FILING DATE: 12-Sep-2003

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/228,213A  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/700,607  
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 199 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: <Unknown>  
; CLONE: Consensus

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-660-946-1

Query Match 71.3%; Score 503; DB 12; Length 199;  
Best Local Similarity 98.1%; Pred. No. 3.9e-50;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
Db 1 MDGQKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
  
Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

RESULT 5

US-09-978-360A-467

; Sequence 467, Application US/09978360A

; Publication No. US20040110939A1

; GENERAL INFORMATION:

; APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueret, Lydie  
; APPLICANT: Jobert, Severin  
; APPLICANT: Clusel, Catherine  
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
; FILE REFERENCE: 56.US4.CIP  
; CURRENT APPLICATION NUMBER: US/09/978,360A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: US 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: US 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: US 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: US 60/099,273  
; PRIOR FILING DATE: -09-04  
; PRIOR APPLICATION NUMBER: US 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: US 09/215,435  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: PCT/IB98/02122  
; PRIOR FILING DATE: 1998-12-17  
; PRIOR APPLICATION NUMBER: US 09/247,155  
; PRIOR FILING DATE: 1999-02-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 810  
; SOFTWARE: Patent.pm  
; SEQ ID NO 467  
; LENGTH: 199  
; TYPE: PRT

; ORGANISM: *Homo sapiens*  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -42..-1  
US-09-978-360A-467

Query Match 71.3%; Score 503; DB 12; Length 199;  
Best Local Similarity 98.1%; Pred. No. 3.9e-50;  
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Ph 1 MDGOKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

## RESULT 6

US-10-466-258-11

; Sequence 11, Application US/10466258

; Publication No. US20040132096A1

**; GENERAL INFORMATION:**

; APPLICANT: GLAXO GROUP LIMITED

; TITLE OF INVENTION: ASSAY

; FILE REFERENCE: P80966 GCW

; CURRENT APPLICATION NUMBER: US/10

; CURRENT FILING DATE: 200

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: P

; SEQ ID NO 1

; LENGTH: 199  
; WIDTH: 80

; TYPE: PRI  
; ORGANISM: U-

Query Match 71.3%; Score 503; DB 16; Length 199;  
Best Local Similarity 98.1%; Pred. No. 3.9e-50;

Pb 1 MDGOKKNWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60

Ov 98 FRIYGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141

<sup>24</sup> See also the discussion of the relationship between the two in the section on the "Economic Crisis."

### RESULTS

RESULT 7

Sequence 8 Application US/10408967

; Sequence 5, Application 35,104  
; Publication No. US20040063161A1

**GENERAL INFORMATION:**

APPLICANT: Pharmacia & Upjohn



Query Match 63.4%; Score 447; DB 9; Length 1163;  
Best Local Similarity 96.9%; Pred. No. 1.3e-42;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| ||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 973 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1032

Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| ||| |||||||||||||||||||||||||||||  
Db 1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1068

RESULT 9  
US-09-789-386-2  
; Sequence 2, Application US/09789386  
; Patent No. US20020010324A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHALOVICH, DAVID  
; APPLICANT: PRINJHA, RABINDER KUMAR  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP-30165-C1  
; CURRENT APPLICATION NUMBER: US/09/789,386  
; CURRENT FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
; PRIOR FILING DATE: 1999-07-19  
; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
; PRIOR FILING DATE: 1998-07-22  
; PRIOR APPLICATION NUMBER: US 09/359,208  
; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-2

Query Match 63.4%; Score 447; DB 9; Length 1192;  
Best Local Similarity 96.98%; Pred. No. 1.4e-42;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| ||||||||||||||||||||||||||||||||||||||  
Db 1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061

Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| ||| |||||||||||||||||||||||||  
Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 10  
US-09-758-140-6  
; Sequence 6, Application US/09758140  
; Patent No. US20020012965A1  
; GENERAL INFORMATION:  
; APPLICANT: Strittmatter, Stephen M.

; TITLE OF INVENTION: No. US20020012965A1 o Receptor-Mediated Blockade of Axonal Growth  
; FILE REFERENCE: 44574-5073-US  
; CURRENT APPLICATION NUMBER: US/09/758,140  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: US 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: US 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-140-6

Query Match 63.4%; Score 447; DB 9; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 1.4e-42;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| |||||||  
Db 1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| |||||  
Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 11

US-09-893-348-23

; Sequence 23, Application US/09893348  
; Patent No. US20020072493A1  
; GENERAL INFORMATION:  
; APPLICANT: EISENBACK-SCHWARTZ, Michal  
; APPLICANT: COHEN, Irun R.  
; APPLICANT: BESERMAN, Pierre  
; APPLICANT: MOSONEGO, Alon  
; APPLICANT: MOALEM, Gila  
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES  
; FILE REFERENCE: EIS-SCHWARTZ=2A  
; CURRENT APPLICATION NUMBER: US/09/893,348  
; CURRENT FILING DATE: 2001-06-28  
; PRIOR APPLICATION NUMBER: US 09/314,161  
; PRIOR FILING DATE: 1999-05-19  
; PRIOR APPLICATION NUMBER: US 09/218,277  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: PCT/US98/14715  
; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 23  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-893-348-23

Query Match 63.4%; Score 447; DB 9; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 1.4e-42;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| ||||||||||||||||||||||||||||||||||||||||||  
Db 1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| ||| |||||||||||||||||||||||||||||||||  
Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 12

US-09-972-599A-6

; Sequence 6, Application US/09972599A  
; Patent No. US20020077295A1  
; GENERAL INFORMATION:  
; APPLICANT: STRITTMATTER, STEPHEN M.  
; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH  
; FILE REFERENCE: C077 CIP US  
; CURRENT APPLICATION NUMBER: US/09/972,599A  
; CURRENT FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: PCT/US01/01041  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/758,140  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/207,366  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/175,707  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-599A-6

Query Match 63.4%; Score 447; DB 9; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 1.4e-42;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| ||||||||||||||||||||||||||||||||||  
Db 1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| ||| |||||||||||||||||||||||||

Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 13

US-10-267-502-429

; Sequence 429, Application US/10267502  
; Publication No. US20040071700A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jaeseob  
; APPLICANT: Galant, Ron  
; TITLE OF INVENTION: Obesity Linked Genes  
; FILE REFERENCE: LSD-07416  
; CURRENT APPLICATION NUMBER: US/10/267,502  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 439  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 429  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-267-502-429

Query Match 63.4%; Score 447; DB 12; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 1.4e-42;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| |||||||

Db 1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061

Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| |||

Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 14

US-10-060-036-71

; Sequence 71, Application US/10060036  
; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yuqiu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060,036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 71  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-060-036-71

Query Match 63.4%; Score 447; DB 14; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 1.4e-42;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| |||||||  
Db 1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| |||  
Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

RESULT 15

US-10-327-213-9

; Sequence 9, Application US/10327213  
; Publication No. US20040121341A1  
; GENERAL INFORMATION:  
; APPLICANT: FILBIN, MARIE T.  
; APPLICANT: DOMENICONI, MARCO  
; APPLICANT: CAO, ZIXUAN  
; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)  
; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION  
; FILE REFERENCE: CUNY/003  
; CURRENT APPLICATION NUMBER: US/10/327,213  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-327-213-9

Query Match 63.4%; Score 447; DB 16; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 1.4e-42;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| |||||||  
Db 1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| |||  
Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

Search completed: September 29, 2004, 18:48:20  
Job time : 16.1353 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:06:43 ; Search time 11.0927 Seconds  
(without alignments)  
4010.587 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:  
1: sp\_archea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp\_rat:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriap:  
17: sp\_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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1	460	65.2	199	13	Q7T224	Q7t224 gallus gall
2	447	63.4	578	11	Q80W95	Q80w95 mus musculu
3	447	63.4	639	11	Q8K290	Q8k290 mus musculu
4	447	63.4	986	4	Q8IUA4	Q8iuu4 homo sapien
5	447	63.4	1046	11	Q8BGK7	Q8bgk7 mus musculu
6	447	63.4	1162	11	Q8BGM9	Q8bgm9 mus musculu
7	443	62.8	356	11	Q8BH78	Q8bh78 mus musculu
8	443	62.8	375	11	Q8BFH5	Q8bfh5 mus musculu
9	443	62.8	392	4	Q96B16	Q96b16 homo sapien
10	436.5	61.9	1163	11	Q8K3G8	Q8k3g8 mus musculu
11	432.5	61.3	357	11	Q8K3G7	Q8k3g7 mus musculu
12	417	59.1	184	6	Q7YRW9	Q7yrw9 bos taurus
13	386	54.8	179	6	Q9GM33	Q9gm33 macaca fasc
14	384	54.5	214	13	Q7T222	Q7t222 carassius a
15	348	49.4	199	4	Q9BQ59	Q9bq59 homo sapien
16	348	49.4	267	11	Q63765	Q63765 rattus sp.
17	337	47.8	780	11	Q8K4S4	Q8k4s4 mus musculu
18	337	47.8	780	11	Q8K0T0	Q8k0t0 mus musculu
19	325	46.1	208	13	Q90637	Q90637 gallus gall
20	320	45.4	760	13	Q90638	Q90638 gallus gall
21	308	43.7	236	11	Q8VBU0	Q8vbu0 rattus norv
22	308	43.7	237	11	Q8C6D5	Q8c6d5 mus musculu
23	308	43.7	643	11	Q8CCU2	Q8ccu2 mus musculu
24	283.5	40.2	221	13	Q7ZUD6	Q7zud6 brachydanio
25	255	36.2	234	5	Q9VMW3	Q9vmw3 drosophila
26	253	35.9	224	5	Q9VMW1	Q9vmw1 drosophila
27	252	35.7	222	5	Q9VMW4	Q9vmw4 drosophila
28	252	35.7	595	5	Q9VMV9	Q9vmv9 drosophila
29	250	35.5	202	5	Q9VMW2	Q9vmw2 drosophila
30	162	23.0	2484	5	Q9U347	Q9u347 caenorhabdi
31	159	22.6	2607	5	Q23187	Q23187 caenorhabdi
32	158	22.4	222	5	Q23188	Q23188 caenorhabdi
33	104	14.8	107	13	Q7T223	Q7t223 carassius a
34	102.5	14.5	154	5	Q9VIB7	Q9vib7 drosophila
35	102.5	14.5	158	5	Q24199	Q24199 drosophila
36	85	12.1	457	10	Q8LDS3	Q8lds3 arabidopsis
37	83.5	11.8	295	3	Q04947	Q04947 saccharomy
38	82.5	11.7	1247	16	Q88QU8	Q88qu8 pseudomonas
39	81.5	11.6	464	5	Q09484	Q09484 caenorhabdi
40	80	11.3	564	10	Q8L7Z9	Q8l7z9 spinacia ol
41	79	11.2	568	16	Q9CKM1	Q9ckm1 pasteurella
42	79	11.2	618	5	Q22003	Q22003 caenorhabdi
43	79	11.2	638	16	Q83F64	Q83f64 coxiella bu
44	78.5	11.1	261	16	Q83KX1	Q83kx1 shigella fl
45	78.5	11.1	458	16	Q9X1C8	Q9xlc8 thermotoga

## ALIGNMENTS

### RESULT 1

#### Q7T224

ID Q7T224 PRELIMINARY; PRT; 199 AA.  
AC Q7T224;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4-C.  
 GN RTN4.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22715887; PubMed=12832288;  
 RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;  
 RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the  
 RT RTN/Nogo gene family.";  
 RL FASEB J. 17:1238-1247(2003).  
 DR EMBL; AY164737; AAP47312.1; -.  
 SQ SEQUENCE 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;  
  
 Query Match 65.2%; Score 460; DB 13; Length 199;  
 Best Local Similarity 88.5%; Pred. No. 6.3e-39;  
 Matches 92; Conservative 5; Mismatches 7; Indels 0; Gaps 0;  
  
 Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
 || | ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1 MDSQPSGWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
  
 Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
 ||||||| ||||| ||||| :||:||:||:||:||:||:||:  
 Db 61 FRIYKGVIQAIQKSDEGHPFRAYLESVDVASEDLIQKYSSVVLG 104

RESULT 2  
 Q80W95  
 ID Q80W95 PRELIMINARY; PRT; 578 AA.  
 AC Q80W95;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Nogo-A (Fragment).  
 GN NOGO-A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tozaki H., Hirata T.;  
 RT "The partial sequence of mouse nogo-A cDNA clone#4109.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AB073672; BAC75974.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 63.4%; Score 447; DB 11; Length 578;

Best Local Similarity 96.9%; Pred. No. 4.4e-37;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 388 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 447  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| ||| | ||||||||||||| ||| ||| ||| ||| |||  
Db 448 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 483

RESULT 3

Q8K290

ID Q8K290 PRELIMINARY; PRT; 639 AA.  
AC Q8K290;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC032192; AAH32192.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 63.4%; Score 447; DB 11; Length 639;  
Best Local Similarity 96.9%; Pred. No. 4.9e-37;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| ||||||||||||||||||||||||||||||||||||||  
Db 449 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 508  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| ||| | ||||||||||||| ||| ||| ||| |||  
Db 509 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 544

RESULT 4

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.  
AC Q8IUA4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE RNT4 (RTN4).  
GN RTN4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Oertle T., van der Putten H., Schwab M.E.;  
RT "Genomic Structure and Functional Characterization of the Promoter  
RT Structures of Human and Mouse Nogo/Rtn-4.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Oertle T., Schwab M.E.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=22376540; PubMed=12488097;  
RA Oertle T., van der Putten H., Schwab M.E.;  
RT "Genomic Structure and Functional Characterization of the Promoter  
RT Structures of Human and Mouse Nogo/Rtn-4.";  
RL J. Mol. Biol. 325:299-323(2003).  
DR EMBL; AY102285; AAM64244.1; -.  
DR EMBL; AY123245; AAM64249.1; -.  
DR EMBL; AY123246; AAM64250.1; -.  
DR EMBL; AY123247; AAM64251.1; -.  
DR EMBL; AY123248; AAM64252.1; -.  
DR EMBL; AY123249; AAM64253.1; -.  
DR EMBL; AY123250; AAM64254.1; -.  
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;  
  
Query Match 63.4%; Score 447; DB 4; Length 986;  
Best Local Similarity 96.9%; Pred. No. 7.9e-37;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 796 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 855  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |  
Db 856 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 891

RESULT 5

Q8BGK7  
ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.  
AC Q8BGK7;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RTN4.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., van der Putten H., Schwab M.E.;  
RT "Genomic Structure and Functional Characterization of the Promoter  
Structures of Human and Mouse Nogo/Rtn-4.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., Schwab M.E.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SvcJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY102280; AAM73502.1; -.  
DR EMBL; AY102286; AAM73507.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 63.4%; Score 447; DB 11; Length 1046;  
Best Local Similarity 96.9%; Pred. No. 8.5e-37;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| |||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 856 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 915  
  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| |||||||||||||||||||||||||||||||||  
Db 916 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 951

RESULT 6  
Q8BGM9  
ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.  
AC Q8BGM9;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RTN4.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090.

CA NCBI\_TAXID\_10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., van der Putten H., Schwab M.E.;  
RT "Genomic Structure and Functional Characterization of the Promoter  
RT Structures of Human and Mouse Nogo/Rtn-4.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., Schwab M.E.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDJB databases.

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SvCJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY102284; AAM73506.1; -.  
DR EMBL; AY102286; AAM73511.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1162 AA: 126613 MW: 855697FBEE11781F CRC64:

Query Match 63.4%; Score 447; DB 11; Length 1162;  
 Best Local Similarity 96.9%; Pred. No. 9.5e-37;  
 Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 7

Q8BH78

ID Q8BH78 PRELIMINARY; PRT; 356 AA.  
AC Q8BH78;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RTN4.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., van der Putten H., Schwab M.E.;  
RT "Genomic Structure and Functional Characterization of the Promoter  
Structures of Human and Mouse Nogo/Rtn-4.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., Schwab M.E.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SvcJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY102281; AAM73503.1; -.  
DR EMBL; AY102286; AAM73508.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 62.8%; Score 443; DB 11; Length 356;  
Best Local Similarity 98.9%; Pred. No. 6.5e-37;  
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 169 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 228

Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 229 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 261

RESULT 8

Q8BHF5

ID Q8BHF5 PRELIMINARY; PRT; 375 AA.  
AC Q8BHF5;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RTN4.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., van der Putten H., Schwab M.E.;  
RT "Genomic Structure and Functional Characterization of the Promoter  
Structures of Human and Mouse Nogo/Rtn-4.";  
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7, and 129SvcJ7;  
RA Oertle T., Schwab M.E.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvcJ7;  
RA Van der Putten H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129SvcJ7;  
RA Van der Putten H., Mir A.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY102282; AAM73504.1; -.  
DR EMBL; AY102286; AAM73509.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 62.8%; Score 443; DB 11; Length 375;  
Best Local Similarity 98.9%; Pred. No. 6.9e-37;  
Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Db 188 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 247  
Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
||||||||||||||||||||||||||||||||

Db 248 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 280

RESULT 9

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.  
AC Q96B16;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein (RTN4).

GN RTN4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Oertle T., Schwab M.E.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=22376540; PubMed=12488097;

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL J. Mol. Biol. 325:299-323(2003).

DR EMBL; BC016165; AAH16165.1; -.

DR EMBL; AY102285; AAM64242.1; -.

DR EMBL; AY102278; AAM64247.1; -.

DR GO; GO:0005783; C:endoplasmic reticulum; IEA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

KW Hypothetical protein.

SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 62.8%; Score 443; DB 4; Length 392;

Best Local Similarity 98.9%; Pred. No. 7.3e-37;

Matches 92; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108

Db 205 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 264  
Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
Db 265 QKSDEGHPFRAYLESEVAISEELVQKYSNSALG 297

RESULT 10

Q8K3G8

ID Q8K3G8 PRELIMINARY; PRT; 1163 AA.  
AC Q8K3G8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Nogo-A.  
GN RTN4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Jin W., Long M., Li R., Ju G.;  
RT "Cloning and expression of the mouse Nogo-A protein.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY114152; AAM77068.1; -.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1163 AA; 126691 MW; 6B5F362799417EA4 CRC64;

Query Match 61.9%; Score 436.5; DB 11; Length 1163;  
Best Local Similarity 95.9%; Pred. No. 1.1e-35;  
Matches 93; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 46 KDKVVVDLLYWRDIKKTGVV-FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 104  
| |||||||||||||| | |||||||||||||||||||||||  
Db 972 KTSVVVDLLYWRDIKKTGVVYFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1031  
Qy 105 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| |||| | ||||| | ||||| | ||||| | ||||| |  
Db 1032 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1068

RESULT 11

Q8K3G7

ID Q8K3G7 PRELIMINARY; PRT; 357 AA.  
AC Q8K3G7;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Nogo-B.

GN RTN4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Jin W., Li R., Long M., Shen J., Ju G.;  
 RT "Cloning and expression of the mouse Nogo-B protein.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY114153; AAM77069.1; - .  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;  
  
 Query Match 61.3%; Score 432.5; DB 11; Length 357;  
 Best Local Similarity 97.9%; Pred. No. 7.7e-36;  
 Matches 92; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
  
 Qy 49 VVDLLYWRDIKKTGVV-FGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 107  
 Db 169 VVDLLYWRDIKKTGVVYFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 228  
  
 Qy 108 IAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
 Db 229 IQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 262

## RESULT 12

Q7YRW9  
ID Q7YRW9 PRELIMINARY; PRT; 184 AA.  
AC Q7YRW9;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RTN4w (Fragment).  
GN RTN4.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22715887; PubMed=12832288;  
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;  
RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the  
RT RTN/Nogo gene family.";  
RL FASEB J. 17:1238-1247(2003).  
DR EMBL; AY164744; AAP47319.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 184 AA; 20671 MW; DE990E03BBAF84A1 CRC64;

RESULT 13

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.  
AC Q9GM33;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
RT libraries.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AB049853; BAB16739.1; -.  
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

```

Query Match           54.8%;  Score 386;  DB 6;  Length 179;
Best Local Similarity 96.4%;  Pred. No. 2e-31;
Matches   81;  Conservative   2;  Mismatches   1;  Indels   0;  Gaps   0;

Y      58 IKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPF 117
       :|||||||||||||||||||||||||||||||||:|||||| ||||||||
D      1 MKKTVVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIQAIQKSDEGHPF 60

Y      118 RAYLESEVAISEELVQKYSNSALG 141
       |||||||||||||||||||||
D      61 RAYLESEVAISEELVQKYSNSALG 84

```

RESULT 14

Q7T222

ID Q7T222 PRELIMINARY; PRT; 214 AA.

AC Q7T222;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4-M.

GN RTN4.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Carassius.

OX NCBI\_TaxID=7957;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22715887; PubMed=12832288;

RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;

RT "A reticular rhapsody: phylogenetic evolution and nomenclature of the

RT RTN/Nogo gene family.";

RL FASEB J. 17:1238-1247(2003).

DR EMBL; AY164754; AAP47329.1; -.

SQ SEQUENCE 214 AA; 24063 MW; E9B603B043159DD9 CRC64;

Query Match 54.5%; Score 384; DB 13; Length 214;  
Best Local Similarity 71.4%; Pred. No. 3.9e-31;  
Matches 70; Conservative 20; Mismatches 8; Indels 0; Gaps 0;

Qy 43 KHWKDKVV DLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYK 102  
Db 21 KHWKEQV DLLYWRDLQRTGVVFGASL LLSLSVCSIISVISYVALALLSVTISFRIYK 80

Qy 103 GVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140  
Db 81 GILQAVQKSEDGHPFKMYLDKDIGHISSELVQKYSDTAL 118

## RESULT 15

## Q9BQ59

DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; IEA.  
DR GO; GO:0006334; P:nucleosome assembly; IEA.  
DR InterPro; IPR001951; Histone\_H4.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS00047; HISTONE\_H4; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 199 AA; 22642 MW; 7CFA44CC568DF6D8 CRC64;

Query Match 49.4%; Score 348; DB 4; Length 199;  
Best Local Similarity 64.0%; Pred. No. 1.7e-27;  
Matches 64; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
|| :|| : :|||||||:||:|||: | || ||| ||:||| ||:||| || |||  
Db 1 MDCVWSNWKSQAIDLLYWRDIKQTGIVFGSFLFFFSLTQFSVVSVVAYLALAALSATIS 60

Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137  
||||| |:|||: | :|||||:||| | : :||| :|||:  
Db 61 FRIYKSVLQAVQKTDEGHPKAYLEITLSQEIQKYTD 100

Search completed: September 29, 2004, 18:19:49  
Job time : 12.0927 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 29, 2004, 18:04:48 ; Search time 2.02133 Seconds  
(without alignments)  
3632.211 Million cell updates/sec

Title: US-09-830-972-32

Perfect score: 705

Sequence: 1 QASGEAGVSCLRENFAVYSV.....ESEVAISEELVQKYSNSALG 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	495	70.2	199	1	RTN4_MOUSE	Q99p72 mus musculu
2	447	63.4	1163	1	RTN4_RAT	Q9jk11 rattus norv
3	447	63.4	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
4	337	47.8	776	1	RTN1_HUMAN	Q16799 homo sapien
5	337	47.8	777	1	RTN1_RAT	Q64548 rattus norv
6	309	43.8	236	1	RTN3_HUMAN	Q95197 homo sapien
7	308	43.7	237	1	RTN3_MOUSE	Q9es97 mus musculu
8	214	30.4	545	1	RTN2_HUMAN	Q75298 homo sapien
9	197	27.9	471	1	RTN2_MOUSE	Q70622 mus musculu
10	77.5	11.0	243	1	T2RD_MOUSE	Q9jka2 mus musculu
11	77.5	11.0	261	1	PHSC_ECOLI	P77409 escherichia
12	75.5	10.7	246	1	T2R8_MOUSE	Q9jka0 mus musculu
13	75.5	10.7	545	1	G6PI_HELPY	Q25781 helicobacte
14	74.5	10.6	545	1	G6PI_HELPJ	Q9zk49 helicobacte
15	74	10.5	268	1	YC73_HAEIN	P44150 haemophilus
16	72	10.2	614	1	S6AC_RABIT	P48055 oryctolagus
17	72	10.2	3511	1	MY15_MOUSE	Q9qzz4 mus musculu

18	71	10.1	346	1	3BHS_VACCC	P21097 v 3 beta-hy
19	71	10.1	346	1	3BHS_VACCV	P26670 v 3 beta-hy
20	70	9.9	960	1	GBR1_MOUSE	Q9wv18 mus musculu
21	70	9.9	961	1	GBR1_HUMAN	Q9ubs5 homo sapien
22	70	9.9	991	1	GBR1_RAT	Q9z0u4 rattus norv
23	69	9.8	315	1	LXD1_PHOLE	P21309 photobacter
24	69	9.8	398	1	PGK_STRPN	Q97s89 streptococc
25	69	9.8	468	1	YDBM_CAEEL	Q19084 caenorhabdi
26	68.5	9.7	238	1	T2RA_MOUSE	Q9jka3 mus musculu
27	68.5	9.7	311	1	HTRB_HAEIN	P45239 haemophilus
28	68.5	9.7	325	1	VP35_VARV	P33059 variola vir
29	68	9.6	184	1	YDB5_SCHPO	Q10358 schizosacch
30	68	9.6	1447	1	DCC_HUMAN	P43146 homo sapien
31	67.5	9.6	324	1	VP35_VACCC	P20497 vaccinia vi
32	67.5	9.6	503	1	LEU1_BUCUM	Q9evh0 buchnera ap
33	67.5	9.6	877	1	SULH_SCHPO	O74377 schizosacch
34	67	9.5	175	1	OLE2_BRANA	P29111 brassica na
35	67	9.5	453	1	SYS_ARCFU	O28244 archaeoglob
36	67	9.5	525	1	SYH_CAEEL	P34183 caenorhabdi
37	67	9.5	756	1	RIR1_HAEIN	P43754 haemophilus
38	66.5	9.4	3174	1	CHAC_HUMAN	Q96rl7 homo sapien
39	66	9.4	253	1	ADH_DROAD	Q00669 drosophila
40	66	9.4	537	1	YCUB_SCHPO	O59831 schizosacch
41	66	9.4	548	1	AMDS_EMENI	P08158 emericella
42	65.5	9.3	182	1	Y696_METJA	Q58107 methanococc
43	65.5	9.3	398	1	ACK1_NEIMB	Q9jym1 neisseria m
44	65.5	9.3	664	1	NTPI_ENTHR	P43439 enterococcu
45	65.5	9.3	880	1	DPO1_BACSU	O34996 bacillus su

#### ALIGNMENTS

RESULT 1

RTN4\_MOUSE

ID RTN4\_MOUSE STANDARD; PRT; 199 AA.

AC Q99P72; Q9CTE3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).

GN RTN4 OR NOGO.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3T3-L1; TISSUE=Adipocyte;

RA Coulson A.C., Craggs P.D., Morris N.J.;

RT "Mouse vp20/RTN4C cDNA.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 170-199 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults (By  
CC similarity).  
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2 (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
CC membrane of the endoplasmic reticulum through 2 putative  
CC transmembrane domains (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=1;  
CC Comment=A number of isoforms may be produced;  
CC Name=1;  
CC IsoId=Q99P72-1; Sequence=Displayed;  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; AF326337; AAK08076.1; -.  
DR EMBL; AK003859; -; NOT\_ANNOTATED\_CDS.  
DR MGD; MGI:1915835; Rtn4.  
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.  
DR GO; GO:0005635; C:nuclear membrane; ISS.  
DR GO; GO:0005515; F:protein binding; ISS.  
DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.  
DR GO; GO:0030517; P:negative regulation of axon extension; ISS.  
DR GO; GO:0007399; P:neurogenesis; IDA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
FT DOMAIN 1 25 CYTOPLASMIC (Potential).

FT TRANSMEM 26 50 POTENTIAL.  
 FT DOMAIN 51 137 LUMENAL (Potential).  
 FT TRANSMEM 138 162 POTENTIAL.  
 FT DOMAIN 163 199 CYTOPLASMIC (Potential).  
 FT DOMAIN 12 199 RETICULON.  
 SQ SEQUENCE 199 AA; 22466 MW; 07BE5D580059ED9C CRC64;  
  
 Query Match 70.2%; Score 495; DB 1; Length 199;  
 Best Local Similarity 97.1%; Pred. No. 2.6e-41;  
 Matches 101; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 Qy 38 MDGQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 97  
 || ||| |||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MDDQKKRWKDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTIS 60  
  
 Qy 98 FRIYKGVIQAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||  
 Db 61 FRIYKGVIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 104

## RESULT 2

### RTN4\_RAT

ID RTN4\_RAT STANDARD; PRT; 1163 AA.  
 AC Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)  
 DE (Glut4 vesicle 20 kDa protein).  
 GN RTN4 OR NOGO.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
 RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;  
 RX MEDLINE=99249816; PubMed=10231557;  
 RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;  
 RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:  
 RT a new member of the reticulon family.";  
 RL Biochim. Biophys. Acta 1450:68-76(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=20129258; PubMed=10667796;  
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
 RA Spillmann A.A., Christ F., Schwab M.E.;  
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
 RT antigen for monoclonal antibody IN-1.";  
 RL Nature 403:434-439(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
 RA Ito T., Schwartz S.M.;  
 RT "Cloning of a member of the reticulon gene family in rat: one of two  
 RT minor splice variants.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

RN [4]  
RP FUNCTION.  
RX MEDLINE=22033691; PubMed=12037567;  
RA GrandPre T., Li S., Strittmatter S.M.;  
RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
RL Nature 417:547-551(2002).  
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults (By  
CC similarity).  
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2 (By  
CC similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
CC membrane of the endoplasmic reticulum through 2 putative  
CC transmembrane domains (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=Nogo-A, NI-220-250;  
CC IsoId=Q9JK11-1; Sequence=Displayed;  
CC Name=2; Synonyms=Nogo-B, Foocen-M1;  
CC IsoId=Q9JK11-2; Sequence=VSP\_005658;  
CC Name=3; Synonyms=Nogo-C, VP20;  
CC IsoId=Q9JK11-3; Sequence=VSP\_005656, VSP\_005657;  
CC Name=4; Synonyms=Foocen-M2;  
CC IsoId=Q9JK11-4; Sequence=VSP\_005659;  
CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic  
CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are  
CC present in dorsal root ganglion, sciatic nerve and PC12 cells  
CC after longer exposure. Isoforms 2 and 3 are detected in kidney,  
CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high  
CC level in skeletal muscle. In adult animals isoform 1 is expressed  
CC mainly in the nervous system.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; AF051335; AAF01564.1; -.  
DR EMBL; AJ242961; CAB71027.1; -.  
DR EMBL; AJ242962; CAB71028.1; -.  
DR EMBL; AJ242963; CAB71029.1; -.  
DR EMBL; AF132045; AAD31019.1; -.  
DR EMBL; AF132046; AAD31020.1; -.  
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.  
DR GO; GO:0005635; C:nuclear membrane; ISS.  
DR GO; GO:0005515; F:protein binding; ISS.  
DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.  
DR GO; GO:0030517; P:negative regulation of axon extension; ISS.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
FT DOMAIN 1 989 CYTOPLASMIC (Potential).

FT	TRANSMEM	990	1010	POTENTIAL.
FT	DOMAIN	1011	1104	LUMENAL (Potential).
FT	TRANSMEM	1105	1125	POTENTIAL.
FT	DOMAIN	1126	1163	CYTOPLASMIC (Potential).
FT	DOMAIN	976	1163	RETICULON.
FT	DOMAIN	33	46	POLY-GLU.
FT	DOMAIN	73	76	POLY-ALA.
FT	DOMAIN	140	145	POLY-PRO.
FT	VARSPLIC	1	964	Missing (in isoform 3). /FTId=VSP_005656.
FT	VARSPLIC	965	975	AVLSAELSKTS -> MDGQKKHWKDK (in isoform 3). /FTId=VSP_005657.
FT	VARSPLIC	173	975	Missing (in isoform 2). /FTId=VSP_005658.
FT	VARSPLIC	192	975	Missing (in isoform 4). /FTId=VSP_005659.
FT	CONFLICT	1130	1131	MISSING (IN REF. 3; AAD31020).
SQ	SEQUENCE	1163 AA;	126386 MW;	8CB894B09E94F0B6 CRC64;

Query Match 63.4%; Score 447; DB 1; Length 1163;  
Best Local Similarity 96.9%; Pred. No. 8.2e-36;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

### RESULT 3

RTN4 HUMAN

ID RTN4\_HUMAN STANDARD; PRT; 1192 AA.  
AC Q9NQC3; Q94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;  
AC Q9Y5U6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).  
GN RTN4 OR NOGO OR ASY OR KIAA0886.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129242; PubMed=10667780;  
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.  
RA Michalovich D., Simmons D.L., Walsh F.S.;  
RT "Inhibitor of neurite outgrowth in humans.";  
RL Nature 403:383-384(2000).  
RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RC TISSUE=Brain;  
RX MEDLINE=21010696; PubMed=11126360;  
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
RT endoplasmic reticulum and reduces their anti-apoptotic activity.";  
RL Oncogene 19:5736-5746(2000).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20237542; PubMed=10773680;  
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
RT 2p14-->2p13 by radiation hybrid mapping.";  
RL Cytogenet. Cell Genet. 88:101-102(2000).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 4).  
RA Jin W.-L., Ju G.;  
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";  
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Placenta, and Skeletal muscle;  
RA Ito T., Schwartz S.M.;  
RT "Cloning of a member of the reticulon gene family in human.";  
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Fibroblast;  
RA Yutsudo M.;  
RT "Isolation of a cell death-inducing gene.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RC TISSUE=Pituitary;  
RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
RA Luo B., Hu R., Chen J.;  
RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
RA Yu J., Han L.H.;  
RT "Novel human cDNA clone with function of inhibiting cancer cell  
RT growth.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Brain;  
RX MEDLINE=99156230; PubMed=10048485;  
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 5:355-364(1998).  
RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RX MEDLINE=20499367; PubMed=11042152;  
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
RT "Cloning and functional analysis of cDNAs with open reading frames for  
RT 300 previously undefined genes expressed in CD34+ hematopoietic  
RT stem/progenitor cells.";  
RL Genome Res. 10:1546-1560(2000).  
RN [12]  
RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
RC TISSUE=Brain;  
RA Mao Y.M., Xie Y., Zheng Z.H.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
RN [13]  
RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).  
RC TISSUE=Testis;  
RA Sha J.H., Zhou Z.M., Li J.M.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
RN [14]  
RP TOPOLOGY.  
RC TISSUE=Brain;  
RX MEDLINE=20129259; PubMed=10667797;  
RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
RT "Identification of the Nogo inhibitor of axon regeneration as a  
RT Reticulon protein.";  
RL Nature 403:439-444(2000).  
RN [15]  
RP FUNCTION.  
RC TISSUE=Brain;  
RX MEDLINE=21069055; PubMed=11201742;  
RA Fournier A.E., Grandpre T., Strittmatter S.M.;  
RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";  
RL Nature 409:341-346(2001).  
RN [16]  
RP REVIEW.  
RX MEDLINE=21888956; PubMed=11891768;  
RA Ng C.E.L., Tang B.L.;  
RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron  
RT regeneration.";  
RL J. Neurosci. Res. 67:559-565(2002).  
CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
CC block the regeneration of the nervous central system in adults.  
CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xL and Bcl-2.  
CC This is likely consecutive to their change in subcellular  
CC location, from the mitochondria to the endoplasmic reticulum,  
CC after binding and sequestration.  
CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xL and Bcl-2.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
CC through 2 putative transmembrane domains.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;  
CC IsoId=Q9NQC3-1; Sequence=Displayed;  
CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;  
CC IsoId=Q9NQC3-2; Sequence=VSP\_005655;  
CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;  
CC IsoId=Q9NQC3-3; Sequence=VSP\_005652, VSP\_005653;  
CC Name=4;  
CC IsoId=Q9NQC3-4; Sequence=VSP\_005654;  
CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
CC widely expressed excepted for the liver. Isoform 3 is expressed in  
CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
CC specific.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -!- CAUTION: Ref.11 sequence differs from that shown due to  
CC frameshifts in positions 1149 and 1156.  
CC -----  
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CC -----  
DR EMBL; AJ251383; CAB99248.1; -.  
DR EMBL; AJ251384; CAB99249.1; -.  
DR EMBL; AJ251385; CAB99250.1; -.  
DR EMBL; AB040462; BAB18927.1; -.  
DR EMBL; AB040463; BAB18928.1; -.  
DR EMBL; AF148537; AAG12176.1; -.  
DR EMBL; AF148538; AAG12177.1; -.  
DR EMBL; AF087901; AAG12205.1; -.  
DR EMBL; AF320999; AAG40878.1; -.  
DR EMBL; AF132047; AAD31021.1; -.  
DR EMBL; AF132048; AAD31022.1; -.

DR EMBL; AB015639; BAA83712.1; -.  
DR EMBL; AF077050; AAD27783.1; -.  
DR EMBL; AF177332; AAG17976.1; -.  
DR EMBL; AB020693; BAA74909.1; -.  
DR EMBL; BC001035; AAH01035.1; -.  
DR EMBL; BC007109; AAH07109.1; -.  
DR EMBL; BC014366; AAH14366.1; -.

Query Match 63.4%; Score 447; DB 1; Length 1192;  
Best Local Similarity 96.9%; Pred. No. 8.4e-36;  
Matches 93; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| |||||||  
Db 1002 KTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1061  
| |||||  
Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSNSALG 141  
| |||||  
Db 1062 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALG 1097

#### RESULT 4

##### RTN1\_HUMAN

ID RTN1\_HUMAN STANDARD; PRT; 776 AA.  
AC Q16799; Q16800; Q16801;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Reticulon 1 (Neuroendocrine-specific protein).  
GN RTN1 OR NSP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-A; RTN1-B AND RTN1-C).  
RC TISSUE=Lung carcinoma;  
RX MEDLINE=93293865; PubMed=7685762;  
RA Roebroek A.J.M., Van de Velde H.J.K., Van Bokhoven A., Broers J.L.V.,  
RA Ramaekers F.C.S., Van de Ven W.J.M.;  
RT "Cloning and expression of alternative transcripts of a novel  
RT neuroendocrine-specific gene and identification of its 135-kDa  
RT translational product.";  
RL J. Biol. Chem. 268:13439-13447(1993).  
RN [2]  
RP ALTERNATIVE SPLICING.  
RX MEDLINE=96429995; PubMed=8833145;  
RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,  
RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;  
RT "Genomic organization of the human NSP gene, prototype of a novel gene  
RT family encoding reticulons.";  
RL Genomics 32:191-199(1996).  
RN [3]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=98228245; PubMed=9560466;  
RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,  
RA Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;

RT "Neuronal differentiation is accompanied by NSP-C expression.";  
 RL Cell Tissue Res. 292:229-237(1998).  
 CC -!-- FUNCTION: May be involved in neuroendocrine secretion or in  
 CC membrane trafficking in neuroendocrine cells.  
 CC -!-- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.  
 CC -!-- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=RTN1-A; Synonyms=NSP-A;  
 CC IsoId=Q16799-1; Sequence=Displayed;  
 CC Name=RTN1-B; Synonyms=NSP-B;  
 CC IsoId=Q16799-2; Sequence=VSP\_005644;  
 CC Name=RTN1-C; Synonyms=NSP-C;  
 CC IsoId=Q16799-3; Sequence=VSP\_005645, VSP\_005646;  
 CC -!-- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES  
 CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C  
 CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.  
 CC -!-- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.  
 CC -!-- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; L10333; AAA59950.1; -.  
 DR EMBL; L10334; AAA59951.1; -.  
 DR EMBL; L10335; AAA59952.1; -.  
 DR PIR; A46583; A46583.  
 DR PIR; I60904; I60904.  
 DR Genew; HGNC:10467; RTN1.  
 DR MIM; 600865; -.  
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.  
 DR GO; GO:0004871; F:signal transducer activity; NAS.  
 DR GO; GO:0030182; P:neuron differentiation; TAS.  
 DR GO; GO:0007165; P:signal transduction; NAS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;  
 KW Phosphorylation.  
 FT TRANSMEM 603 623 POTENTIAL.  
 FT TRANSMEM 726 746 POTENTIAL.  
 FT DOMAIN 589 776 RETICULON.  
 FT DOMAIN 609 612 POLY-LEU.  
 FT VARSPLIC 1 420 Missing (in isoform RTN1-B).  
 FT /FTId=VSP\_005644.  
 FT VARSPLIC 1 568 Missing (in isoform RTN1-C).  
 FT /FTId=VSP\_005645.  
 FT VARSPLIC 569 588 GPGPLGPAPPPLLFLNKQK -> MQATADSTKMDCVWSNW  
 FT KSQ (in isoform RTN1-C).  
 FT /FTId=VSP\_005646.  
 SQ SEQUENCE 776 AA; 83617 MW; CA5B6232353096FE CRC64;

Query Match 47.8%; Score 337; DB 1; Length 776;

Best Local Similarity 67.4%; Pred. No. 3e-25;  
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 105  
| | :|||||||:||:||:| ||| ||:||| |||:||| |||:||| |||:||| |||:  
Db 586 KQKAIDLLYWRDIKQTGIVFGSFLLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSQL 645

Qy 106 QAIAKSDEGHPFRAYLESEVAISEELVQKYSN 137  
||: |:|||||:||| |: :||| :|||:  
Db 646 QAVQKTDEGHPKAYLELEITLSQEIQKYTD 677

RESULT 5

RTN1\_RAT

ID RTN1\_RAT STANDARD; PRT; 777 AA.  
AC Q64548; Q64547;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).  
GN RTN1 OR NSP.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).  
RC STRAIN=Wistar; TISSUE=Brain cortex;  
RX MEDLINE=96386034; PubMed=8793864;  
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,  
RA Georgiev G.P., Buchman V.L.;  
RT "Intracellular compartmentalization of two differentially spliced s-  
RT rex/NSP mRNAs in neurons.";  
RL Mol. Cell. Neurosci. 7:289-303(1996).  
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in  
CC membrane trafficking in neuroendocrine cells.  
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By  
CC similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=RTN1-B; Synonyms=S-RexB;  
CC IsoId=Q64548-1; Sequence=Displayed;  
CC Name=RTN1-S; Synonyms=S-RexS;  
CC IsoId=Q64548-2; Sequence=VSP\_005647, VSP\_005648;  
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND  
CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS  
CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.  
CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL  
CC TYPES.  
CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE  
CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC  
CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN  
CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB  
CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE  
CC HINDBRAIN.  
CC -!- SIMILARITY: Contains 1 reticulon domain.

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CC -----

DR EMBL; U17604; AAC53046.1; -.  
DR EMBL; U17603; AAC53045.1; -.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
FT TRANSMEM 604 624 POTENTIAL.  
FT TRANSMEM 727 747 POTENTIAL.  
FT DOMAIN 590 777 RETICULON.  
FT DOMAIN 610 613 POLY-LEU.  
FT VARSPLIC 1 569 Missing (in isoform RTN1-S).  
FT VARSPLIC 570 589 /FTId=VSP\_005647.  
FT VARSPLIC 570 589 IPGPLGSDLVPPLPFFNKQK -> MQATADSTKMDCVWSNW  
FT KSQ (in isoform RTN1-S).  
FT /FTId=VSP\_005648.  
SQ SEQUENCE 777 AA; 83001 MW; AF7479C50F28D0AC CRC64;

Query Match 47.8%; Score 337; DB 1; Length 777;  
Best Local Similarity 67.4%; Pred. No. 3e-25;  
Matches 62; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 46 KDKVV DLLYWRDIKKTVFGASLFL LLSLT VFSIVS VTA YIAL ALL SVT ISF RIY KGVI 105  
| | :||||| ||||:|||:|||:| | ||| ||| ||:||| |||:||| ||| ||| ||| ||| ||| :|:  
Db 587 KQKAID DLLYWRDIKQTGIVFGSF LLL FSL TQFS VSV VAY LALA AL SAT ISF RIY KSVL 646  
Qy 106 QAI AKSDEGH PFRAY LESEVAI SEEL VQ KYSN 137  
||:| :||| |||:||| |: :||:| :||| :|:  
Db 647 QAVQKT DEGH PFKAY LEIT LSQE QI QKY TD 678

## RESULT 6

### RTN3\_HUMAN

ID RTN3\_HUMAN STANDARD; PRT; 236 AA.  
AC O95197;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like  
DE protein II) (NSPLII).  
GN RTN3 OR NSPL2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RC TISSUE=Retina;  
RX MEDLINE=99265974; PubMed=10331947;  
RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;

RT "Cloning of a novel member of the reticulon gene family (RTN3): gene  
RT structure and chromosomal localization to 11q13.";  
RL Genomics 58:73-81(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;  
RT "Cloning and expression analysis of a cDNA encoding a novel  
RT neuroendocrine-specific protein-like protein 1: NSPL1.";  
RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, Eye, and Lymph;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
CC reticulum (Potential).  
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN  
CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL  
CC RETINA.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -----  
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CC -----  
DR EMBL; AF059524; AAC99319.1; -.  
DR EMBL; AF059529; AAD20951.1; -.  
DR EMBL; AF059525; AAD20951.1; JOINED.  
DR EMBL; AF059526; AAD20951.1; JOINED.  
DR EMBL; AF059527; AAD20951.1; JOINED.  
DR EMBL; AF059528; AAD20951.1; JOINED.  
DR EMBL; AF119297; AAD26810.1; -.  
DR EMBL; BC000634; AAH00634.1; -.  
DR EMBL; BC010556; AAH10556.1; -.

DR EMBL; BC011394; AAH11394.1; -.  
 DR EMBL; BC022993; AAH22993.1; -.  
 DR Genew; HGNC:10469; RTN3.  
 DR MIM; 604249; -.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Transmembrane; Endoplasmic reticulum.  
 FT TRANSMEM 68 88 POTENTIAL.  
 FT TRANSMEM 177 197 POTENTIAL.  
 FT DOMAIN 48 236 RETICULON.  
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCDFB7 CRC64;  
  
 Query Match 43.8%; Score 309; DB 1; Length 236;  
 Best Local Similarity 60.9%; Pred. No. 4.7e-23;  
 Matches 56; Conservative 18; Mismatches 18; Indels 0; Gaps 0;  
  
 Qy 49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108  
   | ||::||:|||| ||| :| :|||| ||::|| :|: |||||||||||| | |||:  
 Db 48 VHDLIFWRDVKKTGFVFGTTLIMLLSAAFSVISVSYLILALLSVTISFRIYKSVIQA 107  
  
 Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140  
   ||:|||||:|||: :: :| | | | :|:  
 Db 108 QKSEEQHPFKAYLDVDITLSSEAFHNYMNAAM 139

RESULT 7  
 RTN3\_MOUSE  
 ID RTN3\_MOUSE STANDARD; PRT; 237 AA.  
 AC Q9ES97;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Reticulon protein 3.  
 GN RTN3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;  
 RT "Cloning and expression profile of a novel mouse cDNA encoding a human  
 RT RTN3 homolog.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum (Potential).  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF195940; AAG31360.1; -.  
 DR EMBL; BC014697; AAH14697.1; -.  
 DR MGD; MGI:1339970; Rtn3.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Transmembrane; Endoplasmic reticulum.  
 FT TRANSMEM 69 89 POTENTIAL.  
 FT TRANSMEM 167 187 POTENTIAL.  
 FT DOMAIN 49 237 RETICULON.  
 SQ SEQUENCE 237 AA; 25428 MW; EB60A0A7AC45F0DE CRC64;  
  
 Query Match 43.7%; Score 308; DB 1; Length 237;  
 Best Local Similarity 59.8%; Pred. No. 6e-23;  
 Matches 55; Conservative 19; Mismatches 18; Indels 0; Gaps 0;  
  
 Qy 49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRYKGVIQAI 108  
 | ||::|||:||| :| :||| ||::|| :|: |||||||||:|| |||:  
 Db 49 VHDLIFWRDVKKTGFGTTLIMLLSAAFSVISVVSYLLALLSVTISFRVYKSVIQAV 108  
  
 Qy 109 AKSDEGHPFRAYLESEVAISEELVQKYSNSAL 140  
 ||:|||||:|||: :: :| | | :|:  
 Db 109 QKSEEQHPFKAYLDVDITLSSEAFHNYMNAAM 140

#### RESULT 8

##### RTN2\_HUMAN

ID RTN2\_HUMAN STANDARD; PRT; 545 AA.  
 AC O75298; O60509;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like  
DE protein 1) (NSPLI).  
GN RTN2 OR NSPL1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.  
RC TISSUE=Lung carcinoma;  
RX MEDLINE=98360096; PubMed=9693037;  
RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;  
RT "cDNA cloning, genomic organization, and expression of the human RTN2  
RT gene, a member of a gene family encoding reticulons.";  
RL Genomics 51:98-106(1998).  
RN [2]  
RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).  
RC TISSUE=Brain;  
RX MEDLINE=98191726; PubMed=9530622;  
RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;  
RT "Molecular cloning of a novel mouse gene with predominant muscle and  
neural expression.";  
RL Mamm. Genome 9:274-282(1998).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
CC reticulum (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=RTN2-A;  
CC IsoId=075298-1; Sequence=Displayed;  
CC Note=Isoform RTN2-C is produced by alternative initiation at  
CC Met-341 of isoform RTN2-A;  
CC Name=RTN2-B;  
CC IsoId=075298-2; Sequence=VSP\_005649;  
CC Event=Alternative initiation;  
CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced  
CC by alternative initiation at Met-1 and Met-341;  
CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL  
CC MUSCLE.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -----  
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CC -----  
DR EMBL; AF004222; AAC32542.1; -.  
DR EMBL; AF004223; AAC32543.1; -.  
DR EMBL; AF004224; AAC32544.1; -.  
DR EMBL; AF038540; AAC14910.1; -.  
DR Genew; HGNC:10468; RTN2.  
DR MIM; 603183; -.  
DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.  
DR GO; GO:0004871; F:signal transducer activity; NAS.  
DR GO; GO:0007165; P:signal transduction; NAS.

DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;  
 KW Alternative initiation.  
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.  
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.  
 FT INIT\_MET 341 341 FOR ISOFORM RTN2-C.  
 FT TRANSMEM 368 388 POTENTIAL.  
 FT TRANSMEM 463 483 POTENTIAL.  
 FT DOMAIN 345 545 RETICULON.  
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).  
 /FTId=VSP\_005649.  
 SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;  
  
 Query Match 30.4%; Score 214; DB 1; Length 545;  
 Best Local Similarity 46.7%; Pred. No. 2.2e-13;  
 Matches 42; Conservative 21; Mismatches 27; Indels 0; Gaps 0;  
  
 QY 48 KVVDLLYWRDIKKTGVVFGASILFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQA 107  
 || |||||:| : :||| : || | ||||| |::|| || ||| |::|: |::||  
 Db 344 KVADLLYWKDTRTSGVVFTGLMVSLLCLLHFSIVSVAHLALLLCGTISLRVYRKVLQA 403  
  
 QY 108 IAKSDEGHPFRAYLESEVAISEELVQKYSN 137  
 : : | :||:||: :: :: | :: | : : |:  
 Db 404 VHRGDGANPFQAYLDVDLTREQTERLSH 433

#### RESULT 9

**RTN2\_MOUSE**  
 ID RTN2\_MOUSE STANDARD; PRT; 471 AA.  
 AC 070622; 070620;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like  
 DE protein 1) (NSPLI).  
 GN RTN2 OR NSPL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.  
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;  
 RX MEDLINE=98191726; PubMed=9530622;  
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;  
 RT "Molecular cloning of a novel mouse gene with predominant muscle and  
 neural expression.";  
 RL Mamm. Genome 9:274-282(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Retina;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum  
CC (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1; Synonyms=Brain;  
CC IsoId=O70622-1; Sequence=Displayed;  
CC Name=2; Synonyms=Muscle;  
CC IsoId=O70622-2; Sequence=VSP\_005650, VSP\_005651;  
CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular  
CC tissues.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -----  
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CC -----  
DR EMBL; AF038537; AAC14906.1; -.  
DR EMBL; AF038537; AAC14907.1; -.  
DR EMBL; AF038538; AAC14908.1; -.  
DR EMBL; AF038539; AAC14909.1; -.  
DR EMBL; AF093624; AAD13195.1; -.  
DR EMBL; BC031370; AAH31370.1; -.  
DR MGD; MGI:107612; Rtn2.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Endoplasmic reticulum; Alternative splicing; Transmembrane.  
FT TRANSMEM 295 315 POTENTIAL.  
FT DOMAIN 272 471 RETICULON.  
FT VARSPlic 1 267 Missing (in isoform 2).  
FT /FTId=VSP\_005650.  
FT VARSPlic 268 271 PLLL -> MGSK (in isoform 2).  
FT /FTId=VSP\_005651.  
SQ SEQUENCE 471 AA; 51346 MW; 9BBD8F372CF63AD3 CRC64;

Query Match 27.9%; Score 197; DB 1; Length 471;

Best Local Similarity 44.3%; Pred. No. 8.6e-12;  
Matches 39; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 49 VVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAI 108  
| |||||:| : :| || : || | ||||| |::|| | ||| |::|: |::|:  
Db 272 VADLLYWKDTRTSGAVFTGLMASLLCLLHFHSIVSVAHLALLGLCATISLRVYRKVLQAV 331

QY 109 AKSDEGHPFRAYLESEVAISEELVQKYS 136  
: | :||:|||: :: :: | :: |  
Db 332 HRGDGTNPFFQAYLMDLTLTREQTERLS 359

RESULT 10

T2RD\_MOUSE

ID T2RD\_MOUSE STANDARD; PRT; 243 AA.  
AC Q9JKA2;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Taste receptor type 2 member 13 (T2R13) (Taste receptor family B  
member 3) (TRB3) (Fragment).  
GN TAS2R13.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DBA/2J;  
RX MEDLINE=20227309; PubMed=10766242;  
RA Matsunami H., Montmayeur J.-P., Buck L.B.,  
RT "A family of candidate taste receptors in human and mouse.";  
RL Nature 404:601-604(2000).  
RN [2]  
RP REVIEW.  
RX MEDLINE=22135574; PubMed=12139982;  
RA Montmayeur J.-P., Matsunami H.;  
RT "Receptors for bitter and sweet taste.";  
RL Curr. Opin. Neurobiol. 12:366-371(2002).  
RN [3]  
RP REVIEW.  
RX MEDLINE=21634924; PubMed=11696554;  
RA Margolskee R.F.;  
RT "Molecular mechanisms of bitter and sweet taste transduction.";  
RL J. Biol. Chem. 277:1-4(2002).  
RN [4]  
RP REVIEW.  
RX MEDLINE=22469025; PubMed=12581520;  
RA Zhang Y., Hoon M.A., Chandrashekhar J., Mueller K.L., Cook B., Wu D.,  
RA Zuker C.S., Ryba N.J.;  
RT "Coding of sweet, bitter, and umami tastes: different receptor cells  
sharing similar signaling pathways.";  
RL Cell 112:293-301(2003).  
CC -!- FUNCTION: Receptor that may play a role in the perception of  
bitterness and is gustducin-linked. May play a role in sensing the  
chemical composition of the gastrointestinal content. The activity  
of this receptor may stimulate alpha gustducin, mediate PLC-beta-2

CC activation and lead to the gating of TRPM5.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells  
CC of the tongue and palate epithelium and exclusively in gustducin-  
CC positive cells.  
CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited  
CC number of bitter compounds; individual taste cells can  
CC discriminate among bitter stimuli.  
CC -!- SIMILARITY: Belongs to family T2R of G-protein coupled receptors.  
CC -----

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DR EMBL; AF247733; AAF64510.1; -.

DR MGD; MGI:1890148; Tas2rl3.

DR InterPro; IPR007960; TAS2R.

DR Pfam; PF05296; TAS2R; 1.

KW Receptor; G-protein coupled receptor; Transmembrane.

FT	NON_TER	1	1	
FT	DOMAIN	<1	12	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	13	33	2 (POTENTIAL).
FT	DOMAIN	34	54	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	55	75	3 (POTENTIAL).
FT	DOMAIN	76	99	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	100	120	4 (POTENTIAL).
FT	DOMAIN	121	150	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	151	171	5 (POTENTIAL).
FT	DOMAIN	172	195	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	196	216	6 (POTENTIAL).
FT	DOMAIN	217	222	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	223	>243	7 (POTENTIAL).
FT	CARBOHYD	128	128	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	NON_TER	243	243	
SQ	SEQUENCE	243 AA;	28110 MW;	D8AD14AF95B9E0B2 CRC64;

Query Match 11.0%; Score 77.5; DB 1; Length 243;

Best Local Similarity 27.1%; Pred. No. 2;

Matches 32; Conservative 18; Mismatches 47; Indels 21; Gaps 5;

Qy 17 VYSVSVGHNLLLEGRSWQEMDGQKKH---WKDKVV DLLYWRDIKKTGVVFGASLFLL 73  
Db :|| : :|| :|| :| | :| :|| || :|| | :|| | :|| |

Db 37 LYSALMTTRKVLIIFNNNSWTVIN---HFNIWLATCLSIFYFLKIAN---FSNSIIFSL 88

Qy 74 SLTVFSIVSVTAYIALALLSV-----TISFRIYKGVIQAIAKSDEG-HPFRAYL 121  
Db | ::|||| :|| || | || :|| :|| | | :|

Db 89 RWRVKTVVSVTLMMSLLL FVNVLINTFIVISVDVYKVNTSYSSHSDNNLHISRIFL 146

RESULT 11

PHSC\_ECOLI

ID PHSC\_ECOLI STANDARD PRT; 261 AA.

AC P77409;

DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE PhsC protein homolog.  
GN YDHU OR B1670.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97175536; PubMed=9023191;  
RA Hensel M., Shea J.E., Baeumler A.J., Gleeson C., Blattner F.R.,  
RA Holden D.W.;  
RT "Analysis of the boundaries of Salmonella pathogenicity island 2 and  
RT the corresponding chromosomal region of Escherichia coli K-12.";  
RL J. Bacteriol. 179:1105-1111(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,  
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,  
RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,  
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,  
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,  
RA Yamamoto Y., Horiuchi T.;  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
CC (Potential).  
CC -!- SIMILARITY: TO S.TYPHIMURIUM PHSC.  
CC -----  
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CC -----  
DR EMBL; AE000262; AAC74740.1; -.  
DR EMBL; U68703; AAB47946.1; -.  
DR EMBL; D90810; BAA15442.1; -.

DR PIR; F64924; F64924.  
 DR EcoGene; EG13955; ydhU.  
 DR InterPro; IPR000516; Ni\_hydr\_CytB.  
 DR Pfam; PF01292; Ni\_hydr\_CYTB; 1.  
 KW Transmembrane; Inner membrane; Complete proteome.  
 FT TRANSMEM 25 45 POTENTIAL.  
 FT TRANSMEM 81 101 POTENTIAL.  
 FT TRANSMEM 108 128 POTENTIAL.  
 FT TRANSMEM 182 202 POTENTIAL.  
 FT TRANSMEM 224 244 POTENTIAL.  
 SQ SEQUENCE 261 AA; 29583 MW; 65CF1A45691A0AF3 CRC64;  
  
 Query Match 11.0%; Score 77.5; DB 1; Length 261;  
 Best Local Similarity 27.6%; Pred. No. 2.2;  
 Matches 29; Conservative 16; Mismatches 43; Indels 17; Gaps 4;  
  
 Qy 22 VGMHNLLLEGRSWQEMD-GQKKHWKDKVVDLLYWRDIKKTGVVFGASLFLLL---SLT 76  
 ::|:|| || | | |::| : | || | : | ||:|| :  
 Db 44 LGLHALLRARGVKKSATDHGEKIYLYSKAVRLWHWSN-----ALLFVLLLASGLIN 94  
  
 Qy 77 VFSIVSVTAYIALALLSVTISFRI---YKGVIQAIAKSDEGHFPR 118  
 |::| || :| : | : | : | | || :|  
 Db 95 HFAMVGATAVKSLVAVHEVCGFLLLACWLGFVLINAVGDNGHHYR 139

RESULT 12  
 T2R8\_MOUSE  
 ID T2R8\_MOUSE STANDARD; PRT; 246 AA.  
 AC Q9JKA0;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Taste receptor type 2 member 8 (T2R8) (Taste receptor family B member  
 DE 5) (TRB5) (Fragment).  
 GN TAS2R8.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=20227309; PubMed=10766242;  
 RA Matsunami H., Montmayeur J.-P., Buck L.B.;  
 RT "A family of candidate taste receptors in human and mouse.";  
 RL Nature 404:601-604(2000).  
 RN [2]  
 RP REVIEW.  
 RX MEDLINE=22135574; PubMed=12139982;  
 RA Montmayeur J.-P., Matsunami H.;  
 RT "Receptors for bitter and sweet taste.";  
 RL Curr. Opin. Neurobiol. 12:366-371(2002).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=21634924; PubMed=11696554;  
 RA Margolskee R.F.;  
 RT "Molecular mechanisms of bitter and sweet taste transduction.";

RL J. Biol. Chem. 277:1-4(2002).  
 RN [4]  
 RP REVIEW.  
 RX MEDLINE=22469025; PubMed=12581520;  
 RA Zhang Y., Hoon M.A., Chandrashekhar J., Mueller K.L., Cook B., Wu D.,  
 RA Zuker C.S., Ryba N.J.;  
 RT "Coding of sweet, bitter, and umami tastes: different receptor cells  
 RT sharing similar signaling pathways.";  
 RL Cell 112:293-301(2003).  
 CC -!- FUNCTION: Receptor that may play a role in the perception of  
 CC bitterness and is gustducin-linked. May play a role in sensing the  
 CC chemical composition of the gastrointestinal content. The activity  
 CC of this receptor may stimulate alpha gustducin, mediate PLC-beta-2  
 CC activation and lead to the gating of TRPM5.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in subsets of taste receptor cells  
 CC of the tongue and palate epithelium and exclusively in gustducin-  
 CC positive cells. Expressed in 15% taste bud cells in circumvallate  
 CC and foliate papillae but only in 2% in fungiform papillae.  
 CC -!- MISCELLANEOUS: Most taste cells may be activated by a limited  
 CC number of bitter compounds; individual taste cells can  
 CC discriminate among bitter stimuli.  
 CC -!- SIMILARITY: Belongs to family T2R of G-protein coupled receptors.  
 CC -----  
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 CC -----  
 DR EMBL; AF247735; AAF64512.1; -.  
 DR MGD; MGI:1890259; Tas2r8.  
 DR InterPro; IPR007960; TAS2R.  
 DR Pfam; PF05296; TAS2R; 1.  
 KW Receptor; G-protein coupled receptor; Transmembrane.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 15 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 16 36 2 (POTENTIAL).  
 FT DOMAIN 37 59 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 60 80 3 (POTENTIAL).  
 FT DOMAIN 81 102 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 103 123 4 (POTENTIAL).  
 FT DOMAIN 124 153 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 154 174 5 (POTENTIAL).  
 FT DOMAIN 175 198 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 199 219 6 (POTENTIAL).  
 FT DOMAIN 220 225 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 226 246 7 (POTENTIAL).  
 FT NON\_TER 246 246  
 SQ SEQUENCE 246 AA; 28430 MW; 8B8F96F8A62E4474 CRC64;

Query Match 10.7%; Score 75.5; DB 1; Length 246;  
 Best Local Similarity 27.1%; Pred. No. 3.3;  
 Matches 32; Conservative 18; Mismatches 47; Indels 21; Gaps 5;

Qy 17 VYSVSVGHNLLLEGRSWQEMDGQKKH---WKDKVVDLLYWRDIKKTGVVFGASLFLLL 73  
 :|| : :|:: || :: | | : : |: | | | |:|| |  
 Db 40 LYSALMTTRKVLIIFNNSWTVIN---HFNIWLATCLSIFYFLMIAN---FSNSIFLSL 91  
 | :||| :| || | || :|| :|| | | :|  
 Qy 74 SLTVFSIVSVTAYIALALLSV-----TISFRIYKGVIQAIAKSDEG-HPFRAYL 121  
 | :||| :| || | || :|| :|| | | :|  
 Db 92 RWRVKTVVSVTLLMSLLLLFVNVLVINTFIVISVDVYKVNTSYSSHSDNNIHISRIFL 149

RESULT 13

G6PI\_HELPY

ID G6PI\_HELPY STANDARD; PRT; 545 AA.  
 AC 025781;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose  
 DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).  
 GN PGI OR HP1166.  
 OS Helicobacter pylori (Campylobacter pylori).  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Helicobacteraceae; Helicobacter.  
 OX NCBI\_TaxID=210;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=26695 / ATCC 700392;  
 RX MEDLINE=97394467; PubMed=9252185;  
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,  
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,  
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,  
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,  
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,  
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,  
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,  
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the gastric pathogen Helicobacter  
 RT pylori.";  
 RL Nature 388:539-547(1997).  
 CC -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-  
 CC phosphate.  
 CC -!- PATHWAY: Involved in glycolysis and in gluconeogenesis.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the GPI family.  
 CC -----  
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 CC -----  
 DR EMBL; AE000622; AAD08211.1; -.  
 DR PIR; F64665; F64665.  
 DR HSSP; Q9N1E2; 1HOX.  
 DR TIGR; HP1166; -.

DR HAMAP; MF\_00473; -; 1.  
 DR InterPro; IPR001672; G6P\_Isomerase.  
 DR Pfam; PF00342; PGI; 1.  
 DR PRINTS; PR00662; G6PISOMERASE.  
 DR PROSITE; PS00765; P\_GLUCOSE\_ISOMERASE\_1; 1.  
 DR PROSITE; PS00174; P\_GLUCOSE\_ISOMERASE\_2; 1.  
 KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.  
 FT ACT\_SITE 382 382 BY SIMILARITY.  
 FT ACT\_SITE 510 510 BY SIMILARITY.  
 SQ SEQUENCE 545 AA; 62487 MW; BDC68D1625190236 CRC64;  
  
 Query Match 10.7%; Score 75.5; DB 1; Length 545;  
 Best Local Similarity 25.3%; Pred. No. 7.5;  
 Matches 37; Conservative 20; Mismatches 44; Indels 45; Gaps 6;  
  
 Qy 23 GMHNLL-----LLEGRSWQEMDGQ---KKHWKDKVVDLLYWRDIKKTGVVFAGSL 69  
 | | :| ::|:|::| |: | ||: || :| | |||  
 Db 411 GHHEILFSNVLAQAAQAFMKGKSYEEALGELFKGLDKDEAKDLAHHR-----VFFGNRP 464  
  
 Qy 70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSD----- 112  
 :| | | | ::| :|| | : :||| | | |  
 Db 465 SNILLLEKISPSNIGALVALYEHKVVF----QGVIWDINSFDQWGVELGKELAVPILQE 519  
  
 Qy 113 -EGHPFRAYLESEVAISEELVQKYSN 137  
 ||| | | :| ::| :| | |  
 Db 520 LEGHKSNAFDSS--TKHLIELYKN 542

RESULT 14  
 G6PI\_HELPJ  
 ID G6PI\_HELPJ STANDARD; PRT; 545 AA.  
 AC Q9ZK49;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose  
 isomerase) (PGI) (Phosphohexose isomerase) (PHI).  
 GN PGI OR JHP1093.  
 OS Helicobacter pylori J99 (Campylobacter pylori J99).  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;  
 OC Helicobacteraceae; Helicobacter.  
 OX NCBI\_TaxID=85963;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99120557; PubMed=9923682;  
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,  
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,  
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.;  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen Helicobacter pylori.";  
 RL Nature 397:176-180(1999).  
 CC -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-  
 CC phosphate.  
 CC -!- PATHWAY: Involved in glycolysis and in gluconeogenesis.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the GPI family.  
CC -----  
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CC -----  
DR EMBL; AE001536; AAD06664.1; -.  
DR PIR; E71851; E71851.  
DR HSSP; Q9N1E2; 1HOX.  
DR HAMAP; MF\_00473; -; 1.  
DR InterPro; IPR001672; G6P\_Isomerase.  
DR Pfam; PF00342; PGI; 1.  
DR PRINTS; PR00662; G6PISOMERASE.  
DR PROSITE; PS00765; P\_GLUCOSE\_ISOMERASE\_1; 1.  
DR PROSITE; PS00174; P\_GLUCOSE\_ISOMERASE\_2; 1.  
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.  
FT ACT\_SITE 382 382 BY SIMILARITY.  
FT ACT\_SITE 510 510 BY SIMILARITY.  
SQ SEQUENCE 545 AA; 62302 MW; 7DB544D95FD1D237 CRC64;

Query Match 10.6%; Score 74.5; DB 1; Length 545;  
Best Local Similarity 25.3%; Pred. No. 9.4;  
Matches 37; Conservative 19; Mismatches 45; Indels 45; Gaps 6;

Qy 23 GMHNLL-----LLEGRSWQEMDGQ---KKHWKDKVVDLLYWRDIKKTGVVFASL 69  
| | :| ::|:|::| |: | ||: || :| | |||  
Db 411 GHHEILFSNVLAQAAQAFMKGKSYYEALGELLSKGLDKDEAKDLAHR----VFFGNRP 464  
  
Qy 70 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSD----- 112  
:| | | ::|:|| |: :||| | | |  
Db 465 SNILLLEKISPSNIGALVALYEHKVFV----QGVIWDINSFDQWGVELGKELAVPILQE 519  
  
Qy 113 -EGHPFRAYLESEVAISEELVQKYSN 137  
| || | :| : |::| | |  
Db 520 LEGHKSNAFYFDSS---TRHLIELYKN 542

RESULT 15  
YC73\_HAEIN  
ID YC73\_HAEIN STANDARD; PRT; 268 AA.  
AC P44150;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical protein HI1273.  
GN HI1273.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*  
RT Rd.";  
RL Science 269:496-512(1995).

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CC -----  
DR EMBL; U32807; AAC22921.1; -.  
DR PIR; F64024; F64024.  
DR TIGR; HI1273; -.  
DR InterPro; IPR000051; SAM\_bind.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 268 AA; 30510 MW; E5B28DA7AADC4D0B CRC64;

Query Match 10.5%; Score 74; DB 1; Length 268;  
Best Local Similarity 25.2%; Pred. No. 5;  
Matches 29; Conservative 15; Mismatches 49; Indels 22; Gaps 4;

Qy 8 VSCLRENFAVYSVGMHNLLLEGRSWQEMDGQKKHWKDVKVDLLYWRDIKKTGVVFGA 67  
   : ||| : | : || : | | | | | : : || : |  
 Db 94 LDCL---AQFKOKFGHLHLLTFH-----KSWADN-----WDDVPLOADVVLAS 132

Qy	68 SLFLLSSL-TVFSIVSVTAYIALALLSVTISFRIYKGVIQAIAKSDEGHPFRAYL 121
	:   : :   :       : :   :   :
Db	133 RSTLVDDLDMMIEKLCAKAKKRVFLTSVTOHFLDEGVFEATGREDIGEPTYIYL 187

Search completed: September 29, 2004, 18:14:57  
Job time : 12.0213 secs